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(54) **COMPOUNDS SUITABLE FOR TREATMENT OF HAEMOPHILIA**

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CPC **A61K 38/37** (2013.01); **A61K 9/0019** (2013.01); **C07K 14/755** (2013.01)

(58) **Field of Classification Search**

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See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to Von Willebrand (VWF) compounds as well as compositions suitable for treatment of blood clotting diseases. The present invention also relates to pharmaceutical compositions, freeze-dried or liquid, comprising (i) a Factor VIII molecule and (ii) a VWF compound.

20 Claims, 12 Drawing Sheets

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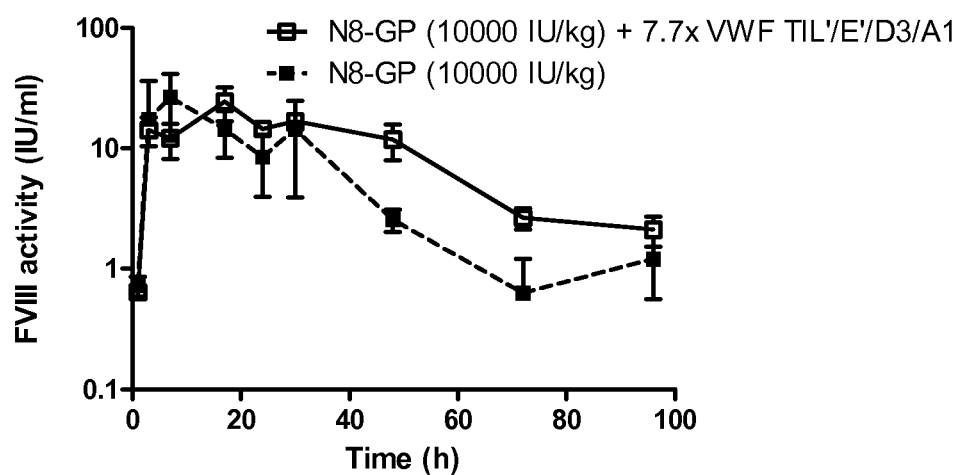


Fig. 1

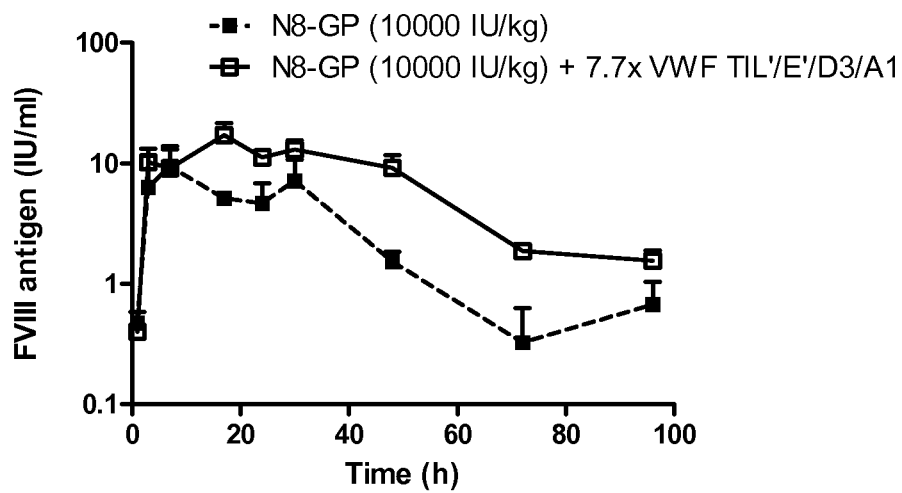


Fig. 2

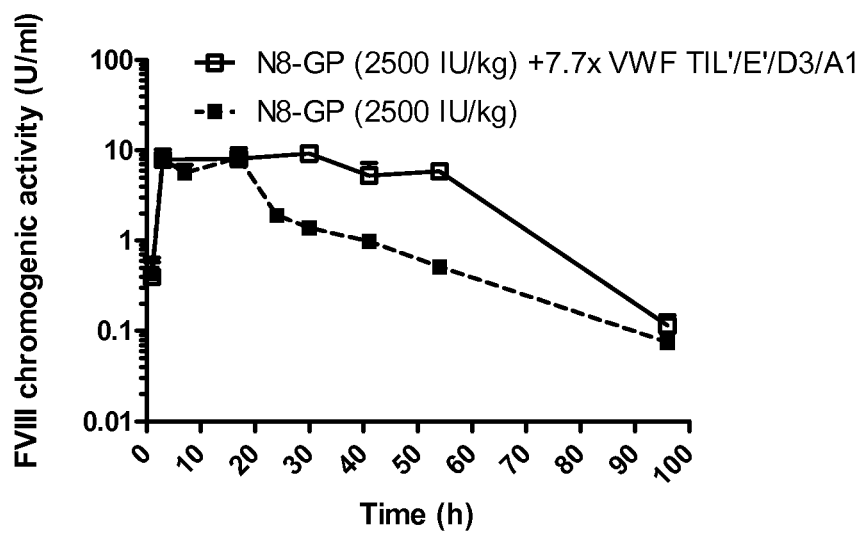


Fig. 3

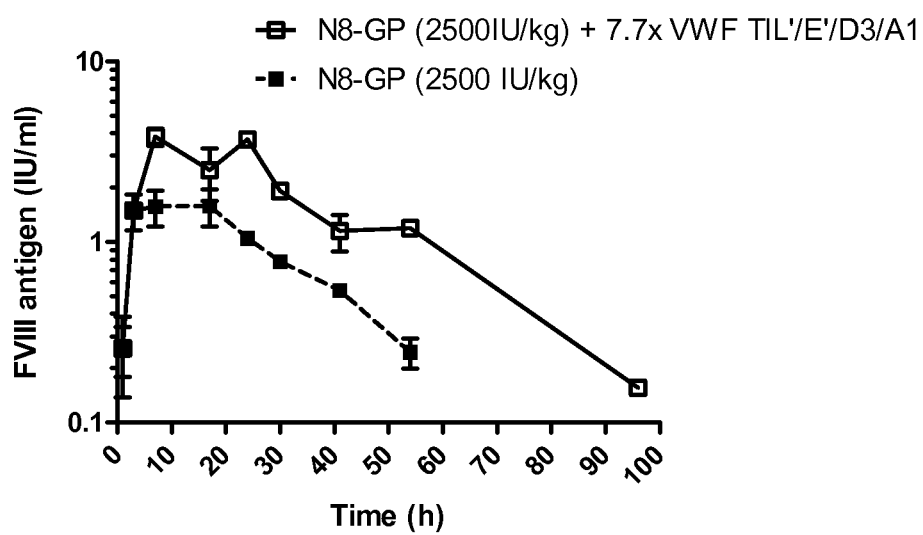


Fig. 4

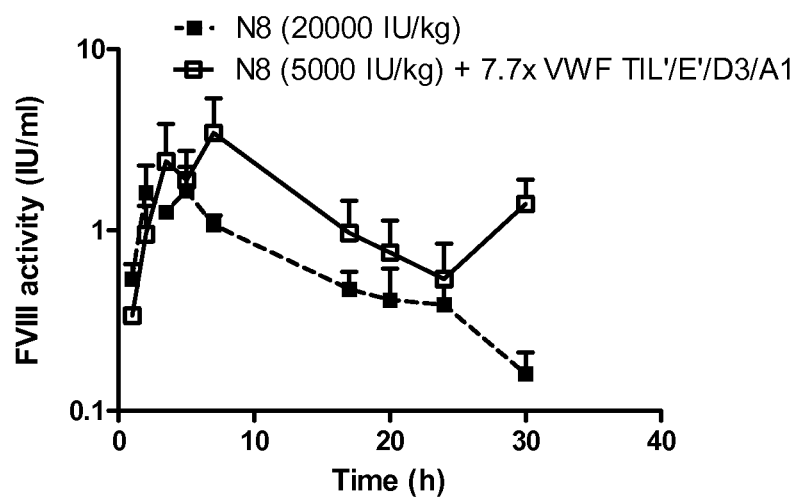


Fig. 5

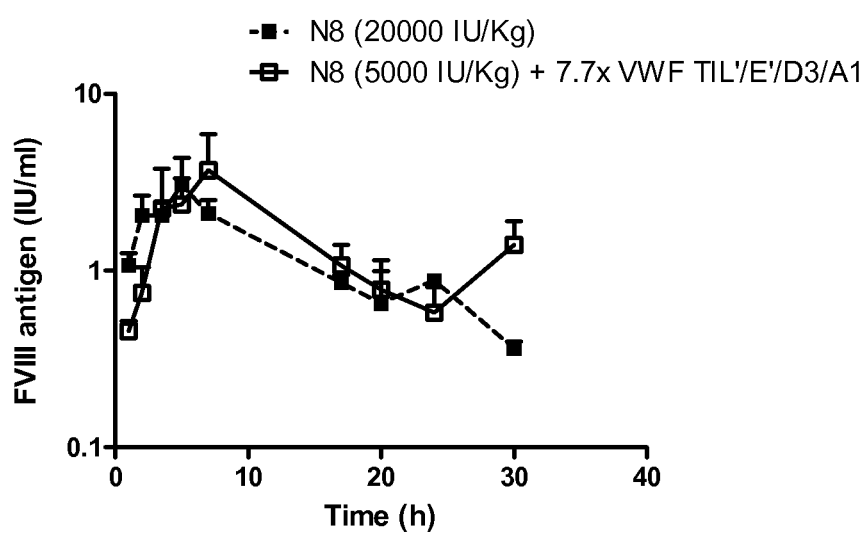


Fig. 6

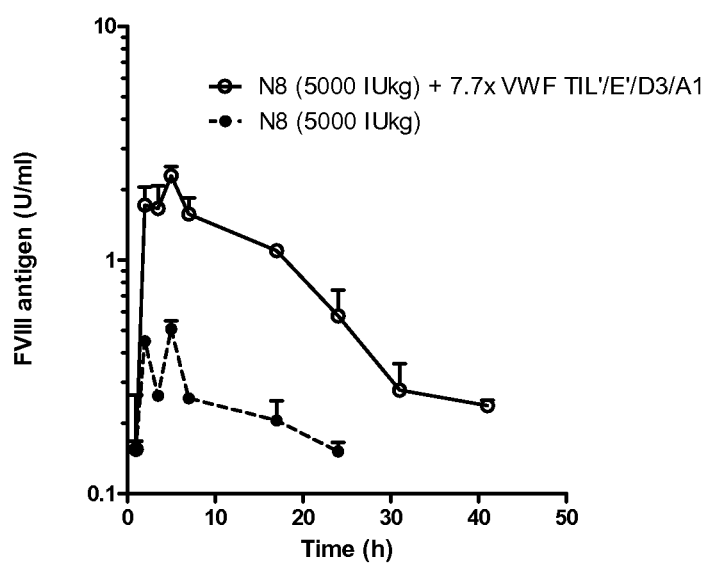


Fig 7

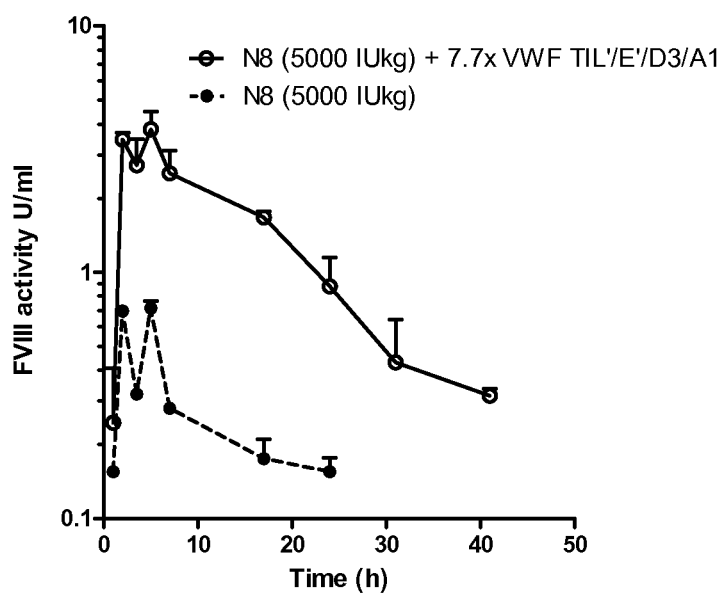


Fig. 8

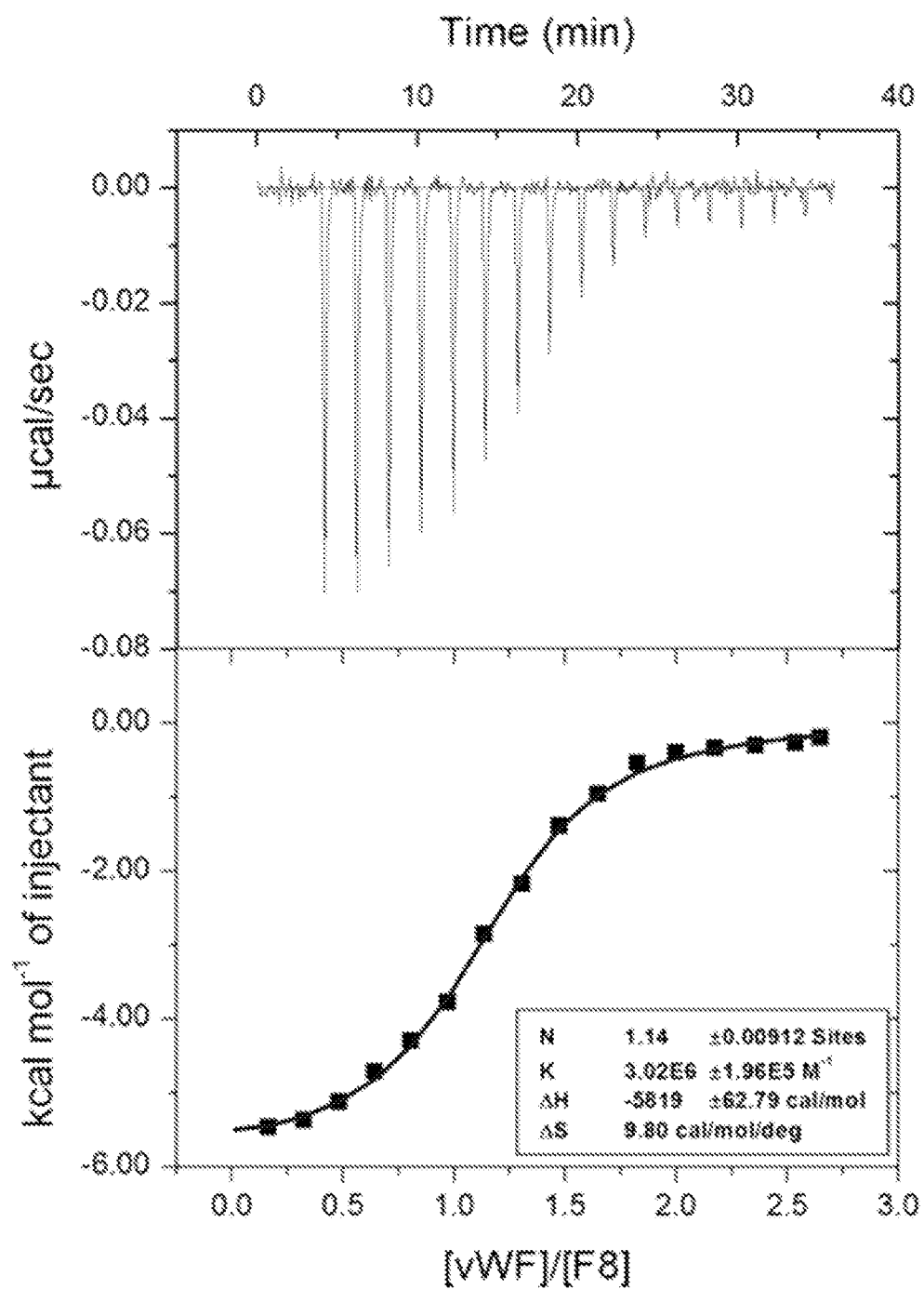


Fig. 9

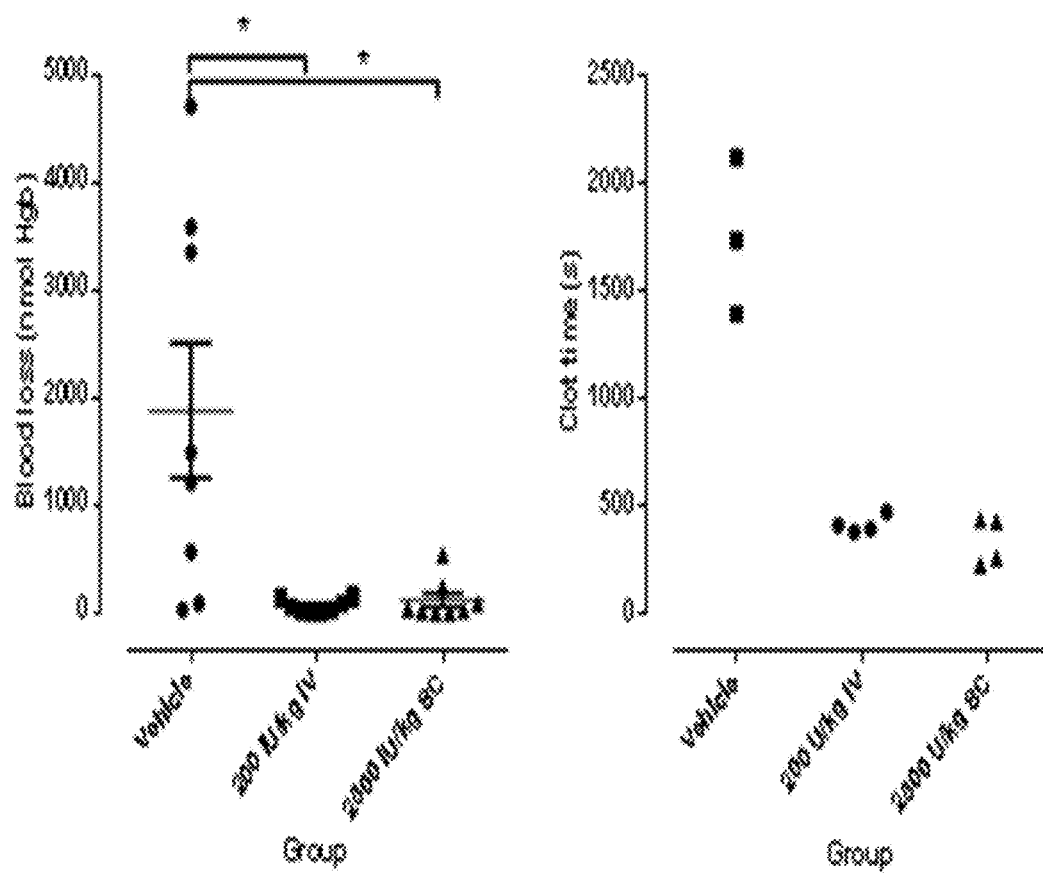


Fig. 10

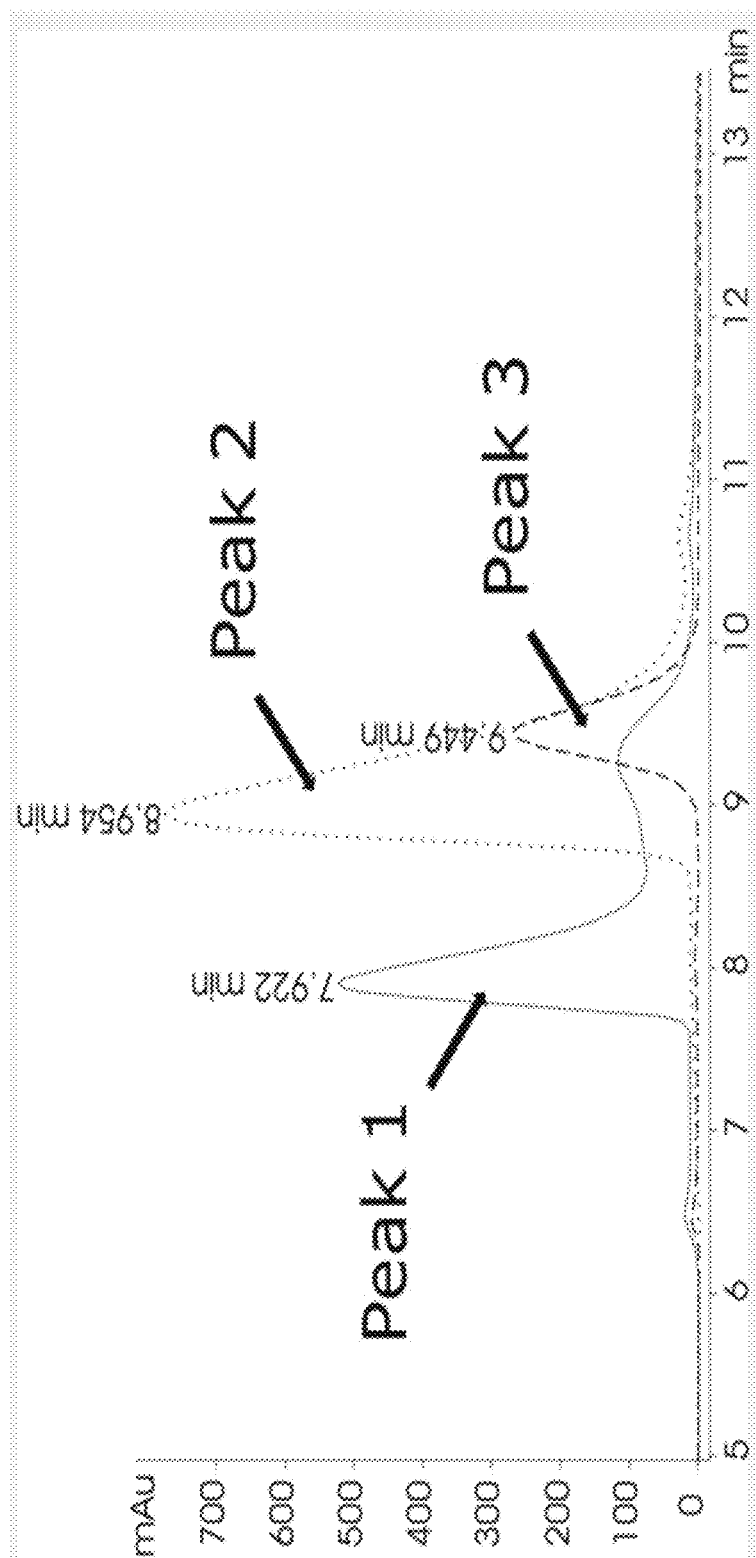


Fig. 11

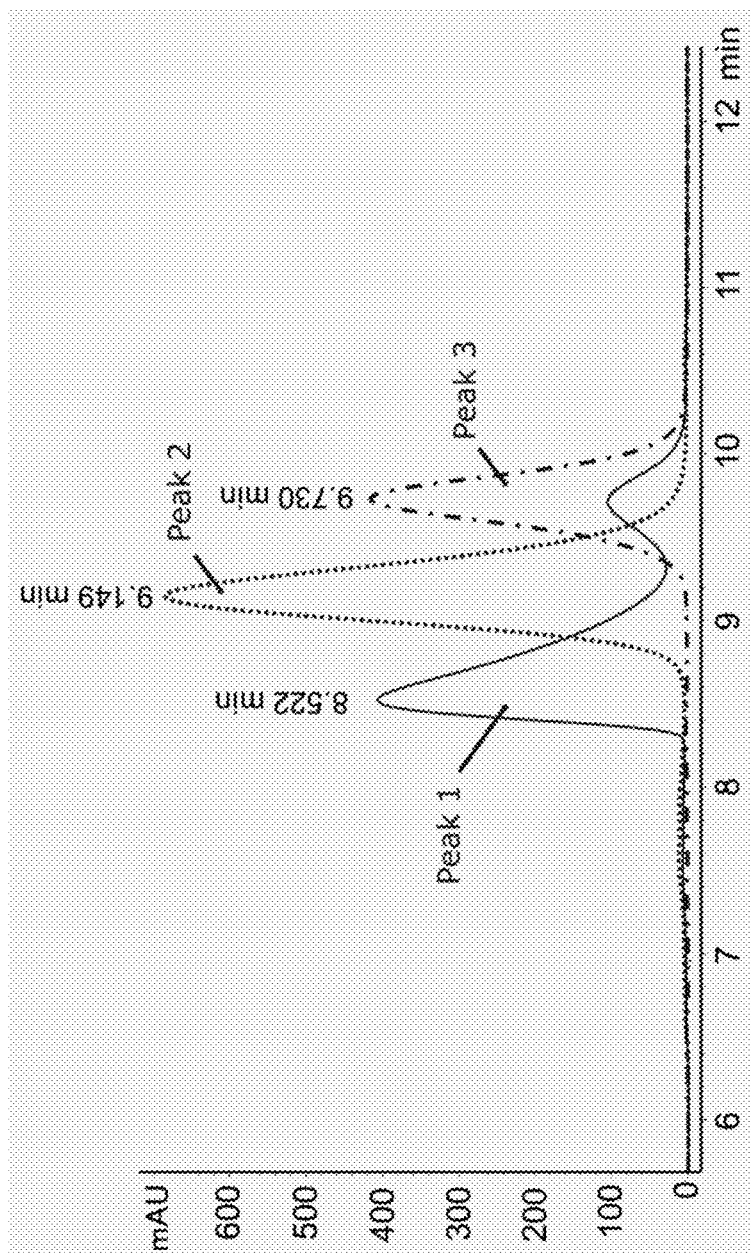


Fig. 12

COMPOUNDS SUITABLE FOR TREATMENT OF HAEMOPHILIA

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of International Application Serial No. PCT/EP2013/055106, filed Mar. 13, 2013, which claimed priority of European Patent Application 12165301.8, filed Apr. 24, 2012 and European Patent Application 13150576.0, filed Jan. 9, 2013; this application also claims priority under 35 U.S.C. §119(e) of U.S. Provisional application 61/641,434, filed May 2, 2012 and U.S. Provisional application 61/752,612, filed Jan. 15, 2013; the contents of all above-named applications are incorporated herein by reference.

TECHNICAL FIELD

The present invention relates to treatment and/or prophylaxis of haemophilia.

BACKGROUND

Protein replacement therapy by intravenous administration of coagulation factors is currently used for treating patients suffering from haemophilia. For patient convenience and compliance, extravascular (e.g. subcutaneous (s.c.) or intradermal) administration would be preferable to the existing intravenous (i.v.) injections. There are furthermore potential safety advantages associated with extravascular administration, since many patients could avoid intravenous port surgery as well as the risk of infection and clots associated with insertion of such catheters.

S.c. administration of FVIII in FVIII deficient mice is disclosed in Shi et al, Haemophilia, 2012, DOI: 10.1111/j.1365-2516.2011.02735.x. The bioavailability of FVIII is herein reported to be low (about 1%).

S.c. administration of FVIII and VWF is furthermore disclosed in WO08151817 but no dose response relationship between the FVIII dose and the achieved circulating FVIII concentration is disclosed. In WO8151817, the (Unit) ratio of VWF over FVIII was larger than 5:1, corresponding to a 150-250 fold molar excess of the concentration of VWF protein as compared to that of FVIII. From a practical and economical point of view, this type of ratios are, however, not desirable. In WO08151817, it is furthermore shown that the immunogenicity in mice of s.c. administered FVIII is significantly reduced when FVIII is co-formulated with VWF.

In WO10062768, it is disclosed that PEGylation of FVIII can improve the bioavailability of FVIII in connection with subcutaneous injection into mice, whereas co-formulation with VWF does not improve the bioavailability of FVIII.

There is a need in the art for compounds and/or pharmaceutical compositions suitable for extravascular administration in treatment and/or prophylaxis of patients suffering from blood clotting diseases such as haemophilia A with or without inhibitors, and/or von Willebrand disease, as such administration forms would alleviate the burden of i.v. treatment both related to the infusion as such and also the risk of infections due to implanted portable catheters. Such compounds and compositions are preferably safe (i.e. have a low risk of immunogenicity) and/or have a high bioavailability and/or are preferably easy to handle in connection with production and formulation processes.

SUMMARY

The present invention relates to a recombinant VWF fragment comprising 1200 amino acids or less, such as e.g. the

TIL' domain or the TIL'/E' domain (Zhou et al. Blood 2012; 120(2): 449-458). The present invention furthermore relates to a pharmaceutical composition comprising: (i) a VWF fragment according to the invention and (ii) FVIII molecule (full-length/truncated B domain/conjugated). The present invention furthermore relates to use thereof for treatment of haemophilia, e.g. by extravascular administration. Such compounds and compositions will preferably result in a relatively high FVIII bioavailability and/or a relatively low risk of FVIII immunogenicity in connection with extravascular co-administration of FVIII.

DESCRIPTION

In one aspect of the invention, VWF fragments according to the invention co-administered with FVIII molecules having a prolonged in vivo circulatory half-life have a surprisingly high bioavailability in connection with extravascular (e.g. s.c.) administration thereof.

The inventors of the present invention have furthermore made the surprising observation that bioavailability of FVIII molecules may be significantly improved upon extravascular co-administration with similar molar amounts of VWF fragments according to the invention. Alternatively, high bioavailability may be achieved through extravascular co-administration of a pool of FVIII molecules, wherein the majority of said FVIII molecules are bound to VWF fragments according to the invention. Interestingly, full length VWF does not have a positive impact on the bioavailability of FVIII. Preferably, VWF should be in the form of a VWF fragment that comprise the TIL' or the TIL'/E' domains. Compounds and compositions according to the present invention are thus useful for treatment and prophylaxis of haemophilia patients (in particular haemophilia A patients) with and without inhibitors, as well as for immune tolerance induction (ITI) of haemophilia patients with inhibitors.

BRIEF DESCRIPTION OF DRAWINGS

FIG. 1: FVIII activity in plasma after subcutaneous administration of 10000 U/kg "N8-GP" with or without co-administration of 7.7 times the molar dose of VWF TIL'/E'/D3/A1 relatively to N8-GP. Data are mean and standard deviation of measurements from n=2 FVIII KO mice per time point. "N8-GP" is a glyco-PEGylated FVIII molecule produced as described in Examples 1+2 in WO2009108806.

FIG. 2: FVIII antigen in plasma after subcutaneous administration of 10000 U/kg N8-GP with or without co-administration of 7.7 times the molar dose of VWF TIL'/E'/D3/A1 relatively to N8-GP. Data are mean and standard deviation of measurements from n=2 FVIII KO mice per time point

FIG. 3: FVIII activity in plasma after subcutaneous administration of 2500 U/kg N8-GP with or without co-administration of 7.7 times the molar dose of VWF TIL'/E'/D3/A1 relatively to N8-GP. Data are mean and standard deviation of measurements from n=2 FVIII KO mice per time point

FIG. 4: FVIII antigen in plasma after subcutaneous administration of 2500 U/kg N8-GP with or without co-administration of 7.7 times the molar dose of VWF TIL'/E'/D3/A1 relatively to N8-GP. Data are mean and standard deviation of measurements from n=2 FVIII KO mice per time point.

FIG. 5: FVIII activity in plasma after subcutaneous administration of 5000 or 20000 IU/kg wt FVIII (N8, turoctocog alfa) with or without co-administration of 7.7 times the molar dose of VWF TIL'/E'/D3/A1 relatively to FVIII, respectively. Data are mean and standard deviation of measurements from n=2 FVIII KO mice per time point. "N8"/"turoctocog alfa" is

a B domain truncated FVIII molecule produced as described in Example 1 in WO2009108806.

FIG. 6: FVIII antigen in plasma after subcutaneous administration of 5000 or 20000 IU/kg wt FVIII (N8, turoctocog alfa) with or without co-administration of 7.7 times the molar dose of VWF TIL'/E'/D3/A1 relatively to FVIII. Data are mean and standard deviation of measurements from n=2 FVIII KO mice per time point.

FIG. 7: FVIII antigen in plasma after subcutaneous administration of 5000 IU/kg FVIII (N8, turoctocog alfa) with or without co-administration of 7.7 times the molar dose of VWF TIL'/E'/D3/A1 relatively to FVIII. Data are mean and standard deviation of measurements from n=2 FVIII KO mice per time point.

FIG. 8: FVIII activity in plasma after subcutaneous administration of 5000 IU/kg FVIII (N8, turoctocog alfa) with or without co-administration of 7.7 times the molar dose of VWF TIL'/E'/D3/A1 relatively to FVIII. Data are mean and standard deviation of measurements from n=2 FVIII KO mice per time point.

FIG. 9: VWF variant (764-865 SEQ ID NO 5) binding to FVIII (N8, turoctocog alfa) at 20° C. The upper panel shows raw data of heat released upon each titration. Lower panel shows binding isotherm obtained from integrating raw data. Data analysis shows that VWF variant (SEQ ID NO 5) binds to FVIII in an exothermic reaction with a stoichiometry of 1.14, ΔH of -5.82 kcal/mole, ΔS of 9.8 cal/mol/deg and a K_d of 0.33 μ M. "F8/N8/turoctocog alfa" is a B domain truncated FVIII molecule produced as disclosed in Example 1 in WO2009108806.

FIG. 10: s.c. administrated N8-GP is haemostatic effective in vivo. The left panel shows blood loss in FVIIIKO mice treated s.c. with N8-GP or vehicle 24 hr before tail transection, or i.v. 5 min before tail transection. N8-GP" is a glyco-PEGylated FVIII molecule produced as described in Examples 1+2 in WO2009108806. The right panel shows clot times in whole blood from the mice ex vivo using ROTEM.

FIG. 11: SEC-UV (280 nm) chromatograms for FVIII, TIL'/E'/D3/A1 III, and a mixture of FVIII and TIL'/E'/D3/A1 III in 155 mM NaCl, 10 mM Calciumacetat, 10% Isopropanol at 25° C.

FIG. 12: SEC-UV (280 nm) chromatograms for FVIII, TIL'/E'/D3 II, and a mixture of FVIII and TIL'/E'/D3 II in 155 mM NaCl, 10 mM Calciumacetat, 10% Isopropanol at 25° C.

DEFINITIONS

The term "treatment", as used herein, refers to the medical therapy of any human or other vertebrate subject in need thereof. Said subject is expected to have undergone physical examination by a medical practitioner, or a veterinary medical practitioner, who has given a tentative or definitive diagnosis which would indicate that the use of said specific treatment is beneficial to treating a disease in said human or other vertebrate. The timing and purpose of said treatment may vary from one individual to another, according to the subject's health. Thus, said treatment may be prophylactic, palliative, symptomatic and/or curative.

Mode of Administration: Compounds and pharmaceutical compositions according to the invention may be administered parenterally, such as e.g. intravenously or extravascularly (such as e.g. intradermally, intramuscularly, subcutaneously, etc). Compounds and pharmaceutical compositions according to the invention may be administered prophylactically and/or therapeutically and/or on demand. According to the present invention, several advantages are associated with extravascular administration of compounds/pharmaceutical

compositions according to the present invention. Extravascular administration is easier, simpler, and associated with less pain, inconvenience, and complications (and thus potentially resulting in better compliance) which is of potential benefit to all patients but of particular benefit for children and small infants.

Combination Treatments/Co-Administration: Combined administration of two or more active compounds (e.g. FVIII and VWF/VWF fragments according to the invention having the ability to bind to FVIII) may be achieved in a number of different ways. In one embodiment, the two active compounds may be administered together in a single composition. In another embodiment, the two active compounds may be administered in separate compositions as part of a combined therapy. For example, the first compound may be administered before, after, or concurrently with the second compound. In case FVIII and VWF fragment are administered extravascularly (e.g. subcutaneously) as two separate pharmaceutical compositions, they are preferably administered in close proximity in order to benefit from the improved bio-availability that can be obtained when administering these two types of compounds together (i.e. the injection sites should be separated by no more than 5 cm, preferably no more than 4 cm, preferably no more than 3 cm, preferably no more than 2 cm, and most preferably no more than 1 cm). The two compounds should preferably also be injected within about an hour, preferably within about 30 minutes, preferably within about 15 minutes, and most preferably within about 5 minutes.

Factor VIII: Factor VIII (FVIII) is a large, complex glycoprotein that is primarily produced by hepatocytes. Human FVIII comprises 2351 amino acids, including a signal peptide, and contains several distinct domains as defined by homology. There are three A-domains, a unique B-domain, and two C-domains. The domain order can be listed as NH₂-A1-A2-B-A3-C1-C2-COOH. The chains are connected by bivalent metal ion-bindings. The A1-A2-B chain is termed the heavy chain (HC) while the A3-C1-C2 is termed the light chain (LC). Small acidic regions C-terminal of the A1 (the a1 region) and A2 (the a2 region) and N-terminal of the A3 domain (the a3 region) play important roles in its interaction with other coagulation proteins, including thrombin and von Willebrand factor (VWF), the carrier protein for FVIII.

Endogenous FVIII molecules circulate in vivo as a pool of molecules with B domains of various sizes, the shortest having C-terminal at position 740, i.e. at the C-terminal of A2-a2, and thus contains no B domain. These FVIII molecules with B-domains of different length all have full procoagulant activity. Upon activation with thrombin, FVIII is cleaved C-terminal of A1-a1 at position 372, C-terminal of A2-a2 at position 740, and between a3 and A3 at position 1689, the latter cleavage releasing the a3 region with concomitant loss of affinity for VWF. The activated FVIII molecule is termed FVIIIa. The activation allows interaction of FVIIIa with phospholipid surfaces like activated platelets and activated factor IX (FIXa), i.e. the tenase complex is formed, allowing efficient activation of factor X (FX).

The terms "Factor VIII(a)" and "FVIII(a)" include both FVIII and FVIIIa. Similarly, the term "Factor VIII" and "FVIII" may include both FVIII and FVIIIa. "Factor VIII" or "FVIII" as used herein refers to a human plasma glycoprotein that is a member of the intrinsic coagulation pathway and is essential to blood coagulation. "Wildtype(wt)/native FVIII" is the human FVIII molecule derived from the full length sequence as shown in SEQ ID NO: 1 (amino acid 1-2332). "FVIII(a)" includes natural allelic variants of FVIII(a) that may exist and occur from one individual to another. FVIII(a)

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may be plasma-derived or recombinantly produced, using well known methods of production and purification. The degree and location of glycosylation, tyrosine sulfation and other post-translation modifications may vary, depending on the chosen host cell and its growth conditions.

Pharmaceutical compositions according to the present invention may comprise native or B domain-truncated FVIII molecules wherein the remaining domains correspond closely to the sequences as set forth in amino acid numbers 1-740 and 1649-2332 of SEQ ID NO: 3. In such molecules, as well as in FVIII comprising the full-length B domain amino acid sequence, mutations may be introduced. Amino acid modifications, such as substitutions, insertions, and deletions, may be introduced into the molecule in order to modify the binding capacity of FVIII with various other components such as low-density lipoprotein receptor-related protein (LRP) and related receptors, various other receptors, other coagulation factors, cell surfaces, introduction and/or abolishment of glycosylation sites, etc. Other mutations that do not abolish FVIII activity may also be accommodated in the FVIII molecules herein.

FVIII molecules herein (molecules/variants/derivatives/analogues/conjugates) are capable of functioning in the coagulation cascade in a manner that is functionally similar, or equivalent, to wt/endogenous FVIII, inducing the formation of FXa via interaction with FIXa on an activated platelet and supporting the formation of a blood clot. FVIII activity can be assessed in vitro using techniques well known in the art. Clot analyses, FX activation assays (often termed chromogenic assays), thrombin generation assays and whole blood thrombo-elastography are examples of such in vitro techniques. FVIII molecules according to the present inven-

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tion have FVIII activity that is at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, 100% or even more than 100% of that of native human FVIII.

Endogenous full length FVIII is synthesized as a single-chain precursor molecule. Prior to secretion, the precursor is cleaved into the heavy chain and the light chain. Recombinant B domain-deleted or truncated FVIII can be produced by means of two different strategies. Either the heavy chain without the B-domain and the light chain are synthesized individually as two different polypeptide chains (two-chain strategy) or the B domain-deleted or truncated FVIII is synthesized as a single precursor polypeptide chain (single-chain strategy) that is cleaved into the heavy and light chains in the same way as the full-length FVIII precursor.

In a B domain-deleted or truncated FVIII precursor polypeptide, produced by the single-chain strategy, the heavy and light chain moieties are often separated by a linker. To minimize the risk of introducing immunogenic epitopes in the B domain-deleted FVIII, the sequence of the linker is preferably derived from the FVIII B-domain. In the B domain of full length FVIII, amino acid 1644-1648 constitutes this recognition site. The thrombin cleavage site leading to removal of the linker on activation of B domain-deleted FVIII is located in the heavy chain. Thus, the size and amino acid sequence of the linker is unlikely to influence its removal from the remaining FVIII molecule by thrombin activation. Deletion/truncation of the B domain is an advantage for production of FVIII. Nevertheless, parts of the B domain can be included in the linker without reducing the productivity. The negative effect of the B domain on productivity has not been attributed to any specific size or sequence of the B domain.

SEQ ID NO: 1: wt human FVIII (Ser750 residue shown in bold and underline)
 ATRRYYLGAVELSWDYMQSDLGELPVDARFPFPRVPSFPFNTSVVYKKTFLVFEFT
 DHLFNIAPRPPMGLLGPTIQAEVYDVTVVITLKNMASHPVSLHAVGVSYWKAEGAEYDD
 QTSQREKEDDKVFPFGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALL
 VCREGSLAKEKTQTLHKFILLFAVFDGKSWHSETKNSLMQDRDAASARAWPKMHTVNGY
 VNRSPLGLIGCHRKSIVYHVGIMGTTPVHSIFLEGHTFLVRNHRQASLEISPIFLTAQTLL
 MDLGQFLFLFCHISSHQHDMGEAYVKVDSCEEPQLRMKNNEEAEDYDDLTDSEMDVVRF
 DDDNSPSFIQIRSVAKKHPKTWHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGR
 KYKKVRFMAYTDTEFTKTRAIQHESGILGPLLYGEVGDTLIIIFKNQASRPYNIYPHGITDVRP
 LYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYSSFVNMRDLASGLI
 GPLLICYKESVDQQRGNQIMSDKRNVLFSVFDENRSWYLTENIQRFLLPNPAGVQLEDPEFQA
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 SGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYEDSYEDISAYLLSKN
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 SPTPHGLSLSDLQEAQYETFSDDPSGAIDSNNLSSEMTHFRPQLHHSMDMVFTEPSGLQL
 RLNEKLGTTAATELKKLDFKVSSTNNLISTIPSDNLAAGTDNTSSLGPPSMFVHYDSQLDTT
 LFGKKSSPLTESGGPLSLSEENNDKLLSGLMNSQESSWGKNVSSTESGRLFKGKRAHG
 PALLTKDNALFKVISISLLKTNKTSNNSATNRKTHIDGPSLLIENSPSVWQNILEDTEFKKVT
 LIHDRMLMDKNATALRLNHMSNKTSSKNMEMVQKKEGPIPPDAQNPDMSEFFKMLFLPES
 ARWIQRTHGKNSLNSGQGPSKQLVSLGPEKSEVGQNFLEKKNKVVGKGEFTKDVGLKE

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MVFPSSRNFLFTNLNDLNHENNTHNQEKKIQEEIEKKETLIQENVVLPQIHTVTGTKNFMKNLF
 LLSTRQNVESGYDGAAYAPVLQDFRSLNDSTNRKKHTAHFSKKGEEENLEGLNQTKQIVE
 KYACTTRISPNTSQQNFVTQRSKRALKQFRLPLEETELEKRIIVDDTSTQWSKNMKHLTPSTL
 TQIDYNEKEKGAITQSPLSDCLTRSHSIPQANRSPLPIAKVSSFPSIRPIYLTRVLFQDNSSHL
 PAASYRKKDSGVQESSHFLQGAKKNNLSLAILTLEMTGDQREVGS LGTSATNSVTYKKVEN
 TVLPKPDLPKTSGBKVELLPKVHIYQKDLFPPTETSNNGSPGHLDLVEGSLQGTGAIKWNEAN
 RPGKVPFLRVATESAKTPSKLLDPLAWDNHYGTQIPKEEWSQEKSPKTAFFKKKDTILSL
 NACESNHAIAAINEGNQKPEIEVTWAKQGRTERLCSQNPVLRKHQRITRITTLQSDQEEID
 YDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLWDYGMSSSPHVLNRQAQS
 GSVPOFKKVVFEFTDGSFTQPLYRGELNEHLGLGPYIRAEVEDNIMVTFRNQASRPYSFY
 SSLISYEEDQRQGAEPKRNFKVPNETKTYFWKVQHMAPTKDEFCKAWAYFSDVDLEKD
 VHSGLIGLLVCHTNTLNPAGRQVTVQEFALFFTI FDETKSWYFTENMERNCRAPCNIQME
 DPTFKENYRPHAINGYIMDTLPGLVMAQDQIRWYLLSMGSNENIHSIHFSGHVFTVRKKEE
 YKMALYNLYPGVFETVEMLPKAGIWRVECLIGEHLHAGMSTLFLVYSNKCQTPGLMASGHI
 RDFQITASGQYQGWAPKLARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGKIQGARQKFS
 SLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNI FNPPIIARYIRLHPHTHSIR
 SLRMELMGCDLNSCSMPLGMESKAISDAQITASSTYFTNMFATWSPSKARLHLQGRSNAW
 RPQVNNPKEWLQVDFQKTMKVTVGTTQGVKSLTSMYVKEFLISSQDGHQWTLFFQNGK
 VKVFQGNQDSFTPVVNSLDPPLLTRYLRHPQSWVHQIALRMEVLGCEAQDLY

The B domain in FVIII spans amino acids 741-1648 of SEQ ID NO: 1. The B domain is cleaved at several different sites, generating large heterogeneity in circulating plasma FVIII molecules. The exact function of the heavily glycosylated B domain is unknown. What is known is that the B domain is dispensable for FVIII activity in the coagulation cascade. Recombinant FVIII is thus frequently produced in the form of B domain-deleted/truncated variants. In a preferred embodiment, the FVIII molecule is produced by an expression vector encoding a FVIII molecule comprising a 21 amino acid residue L (linker) sequence with the following sequence: SEQ ID NO 2: SFSQNSRHPSQNPPVLKRHRQ (the O-glycan is attached to the underlined S). Alternative preferred B domain linker sequences may lack one or more of the amino acid residues set forth in SEQ ID NO 2, e.g. the C-terminal R in SEQ ID NO 2. Preferred FVIII molecules are B domain deleted/truncated variants comprising an O-glycan attached to the Ser 750 residue shown in SEQ ID NO 1—optionally being conjugated to a polymeric (half-life extending) moiety via this O-glycan.

The inventors of the present invention have made the surprising observation that B domain deleted FVIII molecules

according to the invention having a B domain of a size from about 100 to about 400 amino acids ((preferably 150-650, more preferably 150-600, more preferably 150-550, more preferably 150-500, more preferably 150-450, more preferably 150-400, more preferably 150-350, more preferably 200-700, more preferably 200-600, more preferably 200-500, more preferably 200-400, more preferably 200-300, and most preferably about 200 to 250) have a surprisingly high bioavailability in connection with extravascular (e.g. s.c.) administration compared to e.g. FVIII molecules having the entire B domain intact as well FVIII molecules having no or only a few amino acids (e.g. 15-30 amino acids) intact. Such molecules may or may not comprise the Ser750 residue according to SEQ ID NO 1. A simple and safe way of producing FVIII having improved bioavailability upon subcutaneous/intradermal administration is thus provided. It is plausible that the in vivo circulatory half-life of FVIII having B domains of 100 to about 400 amino acids may be prolonged by conjugating/fusing such variants with a half-life extending moiety. An example of a FVIII molecule comprising a 226 amino acid B domain is shown in SEQ ID NO 3:

SEQ ID NO 3: (226 amino acid B domain variant):
 ATRRYLGAVELSWDYMQSDLGELPVDARFPFRVPKSPFNTSVVYKKTLEFVEFT

DHLFNIAKPRPPWMLGLGPTIQAEVYD TVVITLKNMASHPVSLHAVGVS YWKASEGA EYDD

QTSQREKEDDKVPFGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALL

VCREGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGY

VNRSPLGLIGCHRKSVYWHVIGMTTPEVHSIFLEGHTFLVRNHRQASLEISPIITFLTAQTLL

MDLGQFLLFCHISSHQHDGMEAYVKVDSCEEPQLRMKNNEEAEDYDDDLTDEMDVVRF

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DDNNSPSFIQIRSVAKKHPKTWVHYIAAEEEDWDYAPLV LAPDDR SYKSQYLNNGPQRIGR
 KYKKVRFMAYTDETPKTRAIQHESGILGPLLYGEVGD TLLII FKNQASRPYNIYPHGITDVRP
 LYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYSSSFVNMRDLASGLI
 GPLLIC YKESVDQRGNQIMSDKRNVLFSVFDENRSWYL TENIQRFLPNPAGVQLEDPEFQA
 SNIMHSINGYVFDLSQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMVYEDTLTLFPF
 SGETVFMSEMPGLWILGCHNSDFNRGMTALLKVSSCDKNTGDYEDSYEDISAYLLSKN
 NAIEPRSFQNSRHPSTRQKQFNATTIPENDIEKTD PWFARHTPMPKIQNVSSDLLMLLRQ
 SPTPHGLSLSDLQEAKEYTFSDDPSPGAIDSNNSLSEMTFRPQLHHS GDMVFTPE SGLQL
 RLNEKLGTTAATELKKLDFKVSSTSNLISTIPSDNLAAGTDNTSSLGPPSMPVHYDSQLD TT
 LFGKKS SPLTESGGPLSLSEENNDSKLLESGLMNSQESSWGKNVSHHHHHSQNPPVLKR
 HQREITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEENQSPRSFQKKTRHYFIAAVERLW
 DYGMS SSPHVLNRNAQSGSVQFKKVVFEFTDGSFTQPL YRGELNEHLGLLGPYIRAEVE
 DNIMVTFRNQASRPYSFYSSLSIYEEDQRQGAEPKRNFKVPNETKTYFWKVQH HMAPTKDE
 FDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVT VQEFALFFTIFDETSWYF
 TENMERNCRAPCNIQMEDPTFKENYRFHAINGYIMDTLPGLVMAQDQIRIRWYLLSMGSNEN
 IHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETVEMLPSKAGIWRVECLIGEHLHAGMSTLFL
 VYSNKCQTPLGMASGHIRDFQITASGGYQGWAPKLARLHYSGSINAWSTKEFFSWIKVDLL
 APMI IHGIKTQGARQKFSLSYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIF
 NPPIIARYIRLHPHTHYSIRSTLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNM FATW
 SPSKARLHLQGRSNAWRPQVNNPKEWLQVDFQKTMKVTGVT TQGVKSLLTSMYVKEFLIS
 SSQDGHQWTLFFQNGKVKVFQGNQDSFTPVVNSLDP LLLTRYLRIHPQSWVHQIALRMEVL
 GCEAQDLY

Von Willebrand Factor (VWF) is a blood glycoprotein involved in hemostasis. It is deficient or defective in von Willebrand disease which is the most common hereditary bleeding disorder. VWF is a large multimeric glycoprotein present in blood plasma and produced constitutively in endothelium, megakaryocytes, and subendothelial connective tissue. The basic VWF monomer is a 2050 amino acid protein. Each monomer contains a number of specific domains with a specific function, including the TIL' or TIL'/E' domain (Zhou et al. Blood 2012; 120(2): 449-458) which binds to FVIII. FVIII is bound to VWF while inactive in circulation and is released from VWF by the action of thrombin. FVIII(a) not bound to VWF is rapidly cleared and/or degraded. It is shown herein, that full-length VWF does not have the ability to significantly increase bioavailability of extra-vascularly co-administered FVIII despite of its inherent FVIII protective effects.

The full length VWF molecule is thus a very complex protein. The prepro VWF consists of 2813 amino acid residues (SEQ ID NO 22). During secretion, the signal peptide from amino acid residue 1 to 22 and the propeptide from amino acid residue 23 to 763 are cleaved off, leaving a mature VWF of 2050 amino acid residues. The amino acid numbering is thus often based on the prepro VWF and amino acid S764 is thus the first amino acid in the mature molecule. The mature molecule is believed to contain 12 Asn-linked and 10 Thr/Ser linked oligosaccharide side chains. Furthermore this molecule can form dimers, trimers etc. with multimer molecule weight of up to several million Daltons. Different allelic VWF variants are found in human beings and it is thus under-

stood that VWF fragments according to the present invention can be derived from any one of these naturally occurring variants.

The glycosylation heterogeneity, together with the multimer forming properties, of the full length molecule makes it quite challenging to construct an expression system and a downstream purification procedure for a pharmaceutical composition of VWF.

The understanding of the organization and the boundaries of domains in VWF is not yet complete. Only the so-called A domains are well characterized and their crystal structures determined. The chemical assignments of di-sulfides within VWF are limited. However, recent studies on homologies of domains in VWF to domains in and other proteins suggest that several disulfide bonds may be formed. The domain definition of VWF described in Zhou et al. Blood 2012; 120, 449-458 is used herein.

The present invention relates to VWF fragments that are preferably easier to produce than the full length molecule. VWF fragments according to the invention furthermore preferably have the ability to increase bioavailability of s.c. co-administered FVIII. VWF fragments according to the present invention comprise the at least the 15 N-terminal amino acids of the TIL' domain/subdomain (spanning amino acids 764-778 of SEQ ID NO 22) or the TIL' domain/subdomain (spanning amino acids 764-828 of SEQ ID NO 22 or amino acids 764-829 of SEQ ID NO 22) or the TIL'/E' domain/subdomains (spanning amino acids 764-865 of SEQ ID NO 22) and have a size of less than 1500 amino acids, preferably less than 1400 amino acids, preferably less than 1300 amino acids,

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preferably less than 1200 amino acids, preferably less than 1100 amino acids, preferably less than 1000 amino acids, preferably less than 900 amino acids, preferably less than 800 amino acids, preferably less than 700 amino acids, preferably less than 600 amino acids, preferably less than 500 amino acids, preferably less than 400 amino acids, preferably less than 300 amino acids, preferably less than 275 amino acids, preferably less than 250 amino acids, preferably less than 225 amino acids preferably less than 200 amino acids, preferably less than 175 amino acids, preferably less than 150 amino acids, preferably less than 125 amino acids, preferably less than 100 amino acids, preferably less than 95 amino acids, preferably less than 90 amino acids, preferably less than 85 amino acids, or preferably less than 80 amino acids, or preferably less than 75 amino acids, or preferably less than 70 amino acids, or preferably less than 65 amino acids, or preferably less than 60 amino acids, or preferably less than 55 amino acids, or preferably less than 50 amino acids, or preferably less than 45 amino acids, or preferably less than 40 amino acids, or preferably less than 35 amino acids, or preferably less than 30 amino acids, or preferably less than 25 amino acids, or preferably less than 20 amino acids, or preferably less than 15 amino acids. VWF fragments according to the invention preferably comprise the TIL'/E'/D3 domains (where D3 is divided into subdomains VWD3-C8-3-TIL-3-E3) spanning amino acids 764-1250 or amino acids 764-1261 or amino acids 764-1268 of SEQ ID NO 22. VWF fragments according to the invention preferably comprise at least the 15 N-terminal amino acids of TIL', TIL' or TIL'/E' domains (amino acids 764-778, 764-828 or amino acids 764-865 of SEQ ID NO 22). VWF fragments according to the invention may comprise amino acids 764-1242 (SEQ ID NO 57) or amino acids 764-1482 (SEQ ID NO 58). VWF fragments according to the invention may furthermore contain fewer potentially antigenic regions. The molecular weight of VWF fragment dimers according to the present invention may—naturally—be about twice as high as for the monomeric fragments (Dimers according to the present invention may thus comprise up to about 2400 amino acids if the monomer size is 1200 amino acids).

Preferably, the VWF fragments according to the present invention comprise at least amino acids 764-828 (SEQ ID NO 4), or at least amino acids 764-865 (SEQ ID NO 5), or at least amino acids 764-1035 (SEQ ID NO 6), or at least amino acids 764-1041 (SEQ ID NO 7), or at least amino acids 764-1045 (SEQ ID NO 8), or at least amino acids 764-1128 (SEQ ID NO 9), or at least amino acids 764-1198 (SEQ ID no 10), or at least amino acids 764-1250 (SEQ ID NO 11), or at least amino acids 764-1261 (SEQ ID NO 14), or at least amino acids 764-1268 (SEQ ID NO 22), or at least amino acids 764-1242 (SEQ ID NO 57) or at least amino acid 764-1482 (SEQ ID NO 58).

VWF fragments comprising amino acids 764-1242 (SEQ ID NO 57) or amino acid 764-1482 (SEQ ID NO 58) may advantageously have a lower immunogenicity.

In an embodiment, the C1099 and/or the C1142 cysteines may be mutated in the VWF fragments according to the present invention. These cysteine residues are believed to be responsible for the oligomerization/dimerization of the VWF protein. VWF fragments with both cysteines intact may form dimers and homo-oligomers. Modifying both of these cysteines may lead to a product composed of monomer VWF fragments, whereas deletion of one or the other may lead to dimer VWF fragments or potentially to oligomer VWF fragments. Both of the above scenarios may lead to a simpler product purification procedure as compared to the full-length protein.

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In another embodiment, both of the C1099 and C1142 cysteines are kept intact which may lead to a preferentially dimeric VWF fragment. There may be a safety advantage associated with the native sequences incl. the C1099 and the C1142 cysteines.

Surprisingly, co-formulation of FVIII and VWF fragments according to the invention demonstrate improved bioavailability compared to co-formulation of FVIII with a full length VWF molecule. The co-formulations according to the invention show increased bioavailability of Factor VIII when injected subcutaneously. VWF fragments according to the present invention comprise the D' domain (spanning amino acids 764-865/866 of SEQ ID NO: 22) which is thought to be the primary FVIII binding site where FVIII may dock onto D' by electrostatic dipole-dipole like interactions. VWF fragments according to the invention preferably comprise the D' domain and/or the D3-domain (the D3 domain spans amino acids 865/866-1250/1261/1268 of SEQ ID NO: 15). Based on the findings herein, it is possible that both the D' and the D'D3 domains have the ability to bind to FVIII. VWF fragments according to the invention do not to any significant degree (i.e. preferably less than 5%, more preferably less than 4%, preferably less than 3%, preferably less than 2%, more preferably less than 1%) form multimers (i.e., having more than two units, such as e.g. oligomers) because the cysteines (C1099 and C1142) essential for multimer assembly are not present or have been mutated/substituted. Some VWF fragments according to the present invention do furthermore not form dimers to any significant degree—in particular those wherein the C1099 and/or C1142 cysteines are not present.

In some cases, VWF fragments forming dimers may, however, also be useful in connection with the present invention—the TIL'/E'/D3/A1 dimer has e.g. been shown to have a higher FVIII affinity than the monomer. VWF fragment dimers may furthermore be a relatively homogenous product that can be produced relatively easily.

One advantage of the VWF fragments according to the invention is that it is easier to produce such compounds on an industrial scale as a relatively homogenous product due to the low degree of multimerization and due to the fact that the compounds are smaller compounds with fewer posttranslational modifications compared to full length VWF. This means that a high expression level is easier to obtain and/or purification will be less complex due to a less complex molecule. Also, production of recombinant peptides and proteins in simple organisms such as e.g. yeast is a faster and more inexpensive production method compared to production in mammalian cell lines—some VWF fragments according to the present invention can be produced in yeast.

VWF fragments according to the present invention can be in the form of one single VWF fragment (such as e.g. the entire TIL'/E'/D3/A1 region spanning amino acids 764-1459 in SEQ ID NO 22) or alternatively in the form of multiple groups of sequential amino acids from VWF fused together and thus deleting intermediary fragments (such as e.g. a “fusion” of the TIL' and the TIL'/E' domain spanning amino acids 764-828+764-865 in SEQ ID NO 22). Another example could be amino acids 764-828+1127-1197 in SEQ ID NO 22. VWF fragments according to the invention may alternatively be in the form of the repetitive elements. Homologous or heterologous “spacer” sequences may be introduced between the fused VWF fragments/elements (such as e.g. a multiple fusion of TIL'/E' domains such as e.g. TIL'/E'TIL'/E'TIL'/E'). VWF fragments according to the invention may also comprise one or more amino acid alternations (e.g. substitutions, deletions, additions) in the VWF derived sequence(s).

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Bioavailability of FVIII in connection with extravascular co-administration of FVIII and VWF fragments according to the invention may be further improved by conjugating FVIII with at least one half-life extending moiety. It thus follows, that extra-vascular co-administration of VWF fragments comprising the TIL' and/or the TIL'/E' domains with a FVIII molecule conjugated with at least one half-life extending

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moiety is associated with a relatively high FVIII bioavailability.

Examples of VWF fragments according to the present invention (using the domain annotation from Zhou et al.) are shown below in SEQ ID NOs 4-21 and 57-58. TIL'/E'/VWD3 I, TIL'/E'/VWD3 II and TIL'/E'/VWD3 III denote three versions (different lengths) of TIL'/E'/VWD3.

SEQ ID NO 4: amino acids 764-828 (TIL'):
SLSCRPPMVKLVCADNLRAGLECKTKCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCP

SEQ ID NO 5: amino acids 764-865 (TIL'/E'):
SLSCRPPMVKLVCADNLRAGLECKTKCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQG KEYAPGETVK IGCNTCVCQDRKWNCTDHVCA

SEQ ID NO 6: amino acids 764-1035 (TIL'/E'/VWD3 I):
SLSCRPPMVKLVCADNLRAGLECKTKCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVITILVEGGEIELFDGEVNV

KRPMKDETHFEVVESGRYII LLLGKALS VVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQ VEEDPVDFGN SWKVSSQCADTR

SEQ ID NO 7: amino acids 764-1041 (TIL'/E'/VWD3 II):
SLSCRPPMVKLVCADNLRAGLECKTKCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVITILVEGGEIELFDGEVNV

KRPMKDETHFEVVESGRYII LLLGKALS VVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQ VEEDPVDFGN SWKVSSQCADTRKVPLDS

SEQ ID NO 8: amino acids 764-1045 (TIL'/E'/VWD3 III):
SLSCRPPMVKLVCADNLRAGLECKTKCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVITILVEGGEIELFDGEVNV

KRPMKDETHFEVVESGRYII LLLGKALS VVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQ VEEDPVDFGN SWKVSSQCADTRKVPLDSSPAT

SEQ ID NO 9: amino acids 764-1128 (TIL'/E'/VWD3/C8-3) - Cysteine 1099 is marked with bold. This cysteine can be substituted to another amino acid, e.g. Ser:
SLSCRPPMVKLVCADNLRAGLECKTKCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVITILVEGGEIELFDGEVNV

RPMKDETHFEVVESGRYII LLLGKALS VVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRILT

SDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGVVTTWRATL

CPQ

SEQ ID NO 10: amino acids 764-1198 (TIL'/E'/VWD3/C8-3/TIL-3) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser:
SLSCRPPMVKLVCADNLRAGLECKTKCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQGKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVITILVEGGEIELFDGEVNV

KRPMKDETHFEVVESGRYII LLLGKALS VVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

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NNDLTSSNLQVEEDPVDFGN SWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRIL

TSDVPQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGVVWRTA

TLC PQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKIL

DELLQTCVDPEDCPV

SEQ ID NO 11: amino acids 764-1250 (TIL'/E'/D3 I) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser: SLSCRPPMVKLVCADNLRAGLECTKTCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCPCHFQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVTILVEGGEIELFDGEVNV

KRPMKDETHFEVVESEGRYII LLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQVEEDPVDFGN SWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRIL

TSDVPQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGVVWRTA

TLC PQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKIL

DELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVVNLTCEACQEPGGL

VVPPTDA

SEQ ID NO 12: amino acids 864-1250 (D3 I)- Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser: ATCSTIGMAHYLTFDGLKYLFPGEQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK

RVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESEGRYII LLLGKALSVVWDRHLSISVVLKQT

YQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKVPLDSSPATCH

NNIMKQTMVDSSCRILTSDVPQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHV

CAQHGVVWRTATLCPQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQC

VEGCHAHCPPGKILDELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVV

NLTCEACQEPGGL WPPTDA

SEQ ID NO 13: amino acids 864-1268 (D3 II) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser: ATCSTIGMAHYLTFDGLKYLFPGEQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK

RVTILVEGGEIELFDGEVNVKRPMKDETHFEVVESEGRYII LLLGKALSVVWDRHLSISVVLKQT

YQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDFGNSWKVSSQCADTRKVPLDSSPATCH

NNIMKQTMVDSSCRILTSDVPQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHV

CAQHGVVWRTATLCPQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQC

VEGCHAHCPPGKILDELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVV

NLTCEACQEPGGL VVPPTDAPVSPTTLYVEDISEPPLHD

SEQ ID NO 14: amino acids 764-1261 (TIL'/E'/D3 II) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser: SLSCRPPMVKLVCADNLRAGLECTKTCQNYDLECMSMGCVSGCLCPPGMVRHENRCV

ALERCPCHFQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVTILVEGGEIELFDGEVNV

KRPMKDETHFEVVESEGRYII LLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQVEEDPVDFGN SWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRIL

TSDVPQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGVVWRTA

TLC PQSCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKIL

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DELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVVNLTCEACQEPGGL

VVPPTDAPVSPPTLYVED

SEQ ID NO 15: amino acids 764-1264 (TIL'/E'/D3 III) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser:
SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVTILVEGGEIELFDGEVNV

KRPMKDETHFEVVESGRYII LLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQVEEDPVDFGN SWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRIL

TSDVFDQCNKLVDPPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHKGKVVWRTA

TLCQPQSCERNLRENGYECWEYRNSCAPACQVTCQHPEPLACPVQCVGCHAHCPPGKIL

DELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVVNLTCEACQEPGGL

VVPPTDAPVSPPTLYVEDISEP

SEQ ID NO 16: amino acids 764-1268 (TIL'/E'/D3 IV) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser:
SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVTILVEGGEIELFDGEVNV

KRPMKDETHFEVVESGRYII LLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQVEEDPVDFGN SWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRIL

TSDVFDQCNKLVDPPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHKGKVVWRTA

TLCQPQSCERNLRENGYECWEYRNSCAPACQVTCQHPEPLACPVQCVGCHAHCPPGKIL

DELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVVNLTCEACQEPGGL

VVPPTDAPVSPPTLYVEDISEPPLHD

SEQ ID NO 17: amino acids 764-1459 (TIL'/E'/D3/A1 I) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser:
SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVTILVEGGEIELFDGEVNV

KRPMKDETHFEVVESGRYII LLLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQ

NNDLTSSNLQVEEDPVDFGN SWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRIL

TSDVFDQCNKLVDPPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHKGKVVWRTA

TLCQPQSCERNLRENGYECWEYRNSCAPACQVTCQHPEPLACPVQCVGCHAHCPPGKIL

DELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVVNLTCEACQEPGGL

VVPPTDAPVSPPTLYVEDISEPPLHDFYCS RLDDLVLFLD GSSRLSEAEF EVLKAFVVD

MERLRISQKWVRVAVVEYHDSHAYIGLDRKRPSELRI ASQVKYAGSQVASTSEVLKY

TLFQIFSKIDRPEASRITLLMASQEPQMSRNFVRVYQGLKKKKVIVIPVGIGPHANLK

QIRLIEKQAPENKAFVLSSVDELEQQRDEI VSYLCD

SEQ ID NO 18: amino acids 764-1463 (TIL'/E'/D3/A1 II) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser:
SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMGCVSGCLCPPGMVRHENRCV

ALERCPCFHQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVTILVEGGEIELFDGEVNV

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KRPMKDETHFEVVESEGRYII LLLGKALSVVDRHLSISVVLKQTYQEKVCGLCGNFDGIQ
 NNDLTSSNLQVEEDPVDGPN SWKVSSQCADTRKVPLDSSPACHNNIMKQTMVDSSCRIL
 TSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHKGKVVWRTA
 TLC PQSCEERNLRENGYECWEYRNSCAPACQVTCQHPEPLACPVCVEGCHAHCPPGKIL
 DELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVVNLTCEACQEPGGL
 VVPPTDAPVSPPTTLVYEDISEPPLHDFYCS RLLDLVFLLD GSSRLSEAEF EVLKAFVVDM
 MERLRISQKWVRVAVVEYHDGSHAYIGLKDRKRPSELRI ASQVKYAGSQVASTSEVLKY
 TLFQIFSKIDRPEASRITLLMASQEPQMRNFRVRYVQGLKKKVVIVIPVGIGPHANLK
 QIRLIEKQAPENKAFVLSVDELEQQRDEI VSYLCDLAPE

SEQ ID NO 19: amino acids 764-1464 (TIL'/E'/D3/A1 III) - Cysteines
 1099 and 1142 are marked with bold. One or both of these cysteines
 can be substituted to another amino acid, e.g. Ser:
 SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMGCVSGCLCPPGMVRHENRCV

ALERCPCHFQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK
 YLFPGECCYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVTILVEGGEIELFDGEVNV
 KRPMKDETHFEVVESEGRYII LLLGKALSVVDRHLSISVVLKQTYQEKVCGLCGNFDGIQ
 NNDLTSSNLQVEEDPVDGPN SWKVSSQCADTRKVPLDSSPACHNNIMKQTMVDSSCRIL
 TSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHKGKVVWRTA
 TLC PQSCEERNLRENGYECWEYRNSCAPACQVTCQHPEPLACPVCVEGCHAHCPPGKIL
 DELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVVNLTCEACQEPGGL
 VVPPTDAPVSPPTTLVYEDISEPPLHDFYCS RLLDLVFLLD GSSRLSEAEF EVLKAFVVDM
 MERLRISQKWVRVAVVEYHDGSHAYIGLKDRKRPSELRI ASQVKYAGSQVASTSEVLKY
 TLFQIFSKIDRPEASRITLLMASQEPQMRNFRVRYVQGLKKKVVIVIPVGIGPHANLK
 QIRLIEKQAPENKAFVLSVDELEQQRDEI VSYLCDLAPEA

SEQ ID NO 20: amino acids 764-1683 (TIL'/E'/D3/A1/A2) - Cysteines
 1099 and 1142 are marked with bold. One or both of these cysteines
 can be substituted to another amino acid, e.g. Ser:
 SLSCRPPMVKLVCPADNLRAEGLECTKTCQNYDLECMGCVSGCLCPPGMVRHENRCV

ALERCPCHFQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK
 YLFPGECCYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVTILVEGGEIELFDGEVNV
 KRPMKDETHFEVVESEGRYII LLLGKALSVVDRHLSISVVLKQTYQEKVCGLCGNFDGIQ
 NNDLTSSNLQVEEDPVDGPN SWKVSSQCADTRKVPLDSSPACHNNIMKQTMVDSSCRIL
 TSDVFQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHKGKVVWRTA
 TLC PQSCEERNLRENGYECWEYRNSCAPACQVTCQHPEPLACPVCVEGCHAHCPPGKIL
 DELLQTCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVVNLTCEACQEPGGL
 VVPPTDAPVSPPTTLVYEDISEPPLHDFYCS RLLDLVFLLD GSSRLSEAEF EVLKAFVVDM
 MERLRISQKWVRVAVVEYHDGSHAYIGLKDRKRPSELRI ASQVKYAGSQVASTSEVLKY
 TLFQIFSKIDRPEASRITLLMASQEPQMRNFRVRYVQGLKKKVVIVIPVGIGPHANLK
 QIRLIEKQAPENKAFVLSVDELEQQRDEIVSYLCDLAPEAPPTLPPDMAQVTVGPGLGV
 STLGPKRNSMVLDAFVLEGS DKIGEADFNRSEFMEEVIRMDVGGDS IHVTVLQYSYMV
 TVEYFPSEAQSKGIDILQRVREIRYQGGNRTNTGLALRYLSDHSFLVSQGDREQAPNLVYMV
 TGNPASDEIKRLPGDIQVVPVIGVGNANVQELERIGWPNAPILIQDFETLPREAPDLVLQRCC
 SGE GLQIPTLSPA

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SEQ ID NO 21: amino acids 764-1873 (TIL'/E'/D3/A1/A2/A3) - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser:
SLSCRPPMVKLVCPADNLRAGLECTKTCQNYDLECMMSGCVSGCLCPPGMVRHENRCV

ALERCPCHFQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK
YLFPGECCQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKK RVTILVEGGEIELFDGEVNV
KRPMKDETHFEVVESGRYII LLLGKALSVVDRHLSISVVLKQTYQEKVCGLCGNFDGIQ
NNDLTSSNLQVEEDPVDPGN SWKVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRIL
TSDVFQDCNKLVDPEPYLDVCIYDTCSCEISGDCACFCDTIAAYAHVCAQHKGKVVWRTA
TLC PQSCEERNLRENGYEC EWRYNSCAPACQVTCQHPEPLACPVCVEGCHAHCPPGKIL
DELLQTCVDPEDCPVCEVAGRFRFASGKKVTLNPSDPEHCQ ICHCDVNVLTCEACQEPGGL
VVPPTDAPVSPPTLYVEDISEPPLHDFYCS RLLDLVFLD GSSRLSEAEF EVLKAFVVD
MERLRISQKWVRVAVVEYHDGSHAYIGLKDRKRPSLRRI ASQVKYAGSQVASTSEVLKY
TLFQIFSKIDRPEASRITLLMASQEPQRM SRNFVRYVQGLKKKVIPIVIGIGPHANLKQIRLI
EKQAPENKAFVLSSVDELEQQRDEIVSYLCDLAPEAPPPTLPPDMAQVTVGPGLLGVSTLG
PKRNSMVLDAFVLEGS DKIG EADFNRSKEFMEEVIQRM DVGQDSIHVTVLQYSYMTVEY
PFSEAQSKGDILOVRREIRYQGGNRTNTGLALRYLSDHSFLVSQGDREQAPNLVYMTGNP
ASDEIKRLPGDIQVPIGVGPANVQELERIGWPNAPILIQDFETLPREAPDLVLRCCSGEG
LQIPTLSPAPDCSQPLDVILLLDGSSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVL
QYGSITITIDVFNWVPEKAHLLSLVDVMQREGGPSQIGDALGFAVRYLTSEM HGARPGAS
KAVVILVTDVSDVDAADAARSNRVTVPPIGIDRYDAAQLRILAGPAGDSNVVKLQRIED
LPTMVTLGNSFLHKLCS

SEQ ID NO 22: wild-type human VWF according to the UniProtKB/Swiss-Prot database (entry P04275) - cysteine residues at positions 1099 and 1142 are marked with bold:

MIPARFAGVLLALALILPGTLCAEGTRGRSSTARCSLFGSDFVNTFDGSMYSFAGYCSYLLA
GGCQKRFSIIIGDFQNGKRVLSVYLGEFFDIHLFVNGTVTQGDQRVSMYPYASKGLYLETEA
GYKLSGEAYGFVARIDSGSNFQVLLSDRYFNKTCGLCGNFNIFAEDDFMTQEGTLTSDPY
DFANSWALSSGEQWCERASPPSSSCNISSGEMQKGLWEQCQLLKSTSVFARCHPLVDPE
PFVALCEKTLCECAGGLECACPALLEYARTCAQEGMVLYGWTDSACSVPVPAGMEYRQC
VSPCARTCQSLHINEMCQERCVDGCSCEGQLLDEGLCVESTECPCVHSGKRYPPGTSLS
RDCNTCICRNSQWICSNEECPEGELVTGQSHFKSFDNRYFTFSGICQYLLARDCQDHSFSI
VIETVQCADDRDAVCTRSVTVRLPGLHNSLVKLKHGAGVAMDGQDVQLPLKGLDLRIQHTV
TASVRLSYGEDLQMDWDGGRLLVKLSPVYAGKTCGLCGNYNGNQGD DFLTPSGLAEPR
VEDFGNAWKLHGCDQLQKHSDPCALNPRMTRFSEEACAVLTSPTFEACHRAVSPLPYL
RNCRYDVCSCSDGRECLGALASYAAACAGRGVRVAWREPGRCLENC PKGQVYLQCGTP
CNLTCSRSLSPDEECNEACLEGCFPPGLYMDERGD CVPKAQCPCYYDGEIFQPEDIFSDH
HTMCYCEDGFMHCTMSGVPGSLLPDAVLSSPLSHRSKRSLSCRPPMVKLVCPADNLRAG
LECTKTCQNYDLECMMSGCVSGCLCPPGMVRHENRCVALERCPCHFQKEYAPGETVKI
GCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLKYLFPGECCQYVLVQDYCGSNPGT
FRILVGNKGCSHPSVKCKKRVITILVEGGEIELFDGEVNVKRPMKDETHFEVVESGRYII LLLG
KALSVVDRHLSISVVLKQTYQEKVCGLCGNFDGIQNNDLTSSNLQVEEDPVDPGNSWKVS
SQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRIL TSDVFQDCNKLVDPEPYLDVCIYDTCS
CESIGDCACFCDTIAAYAHVCAQHKGKVVWRTATLCPQSCEERNLRENGYEC EWRYNSCA

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PACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDELLQTCVDPEDCPVCEVAGRRFASGK
 KVTLNPSDPEHCQICHCDVNNLTCEACQEPGGLVVPPTDAPVSPPTLYVEDISEPPLHDFYC
 SRLLDLVFLLDGSSRLSEAEFEVLKAFVDDMMERLRISQKWVRVAVVEYHDGSHAYIGLKDR
 KRPSLRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRITLLLMASQEPQRMARNF
 VRYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVLSSVDELEQQORDEIVSYLCDLA
 PEAPPPTLPPDMAQVTVGPGLGVSTLGPKRNSMVLDAFVLEGSCKIGEADFNRSKEFME
 EVIQRMDVGQDSIHVTVLQYSYMTVEYPFSEAQSKGDILQVRVREIRYQGGNRTNTGLALR
 YLSDHSFLVSQGDREQAPNLVYMTGNPASDEIKRLPGDIQVVPVIGVGNANVQELERIGW
 PNAPILIQDFETLPREAPDLVLQRCCSGEGLQIPTLSPAPDCSQPLDVILLDGGSSFPASYFD
 EMKSFAPAFISKANIGPRLTQVSVLQYGSITTIDVPWNVPEKAHLLSLVDVMQREGGPSQIG
 DALGFAVRYLTSEMHGARGPASKAVVILVTDVSVDSVDAADAARSNRVTVFPVIGIGDRYDA
 AQLRILAGPAGDSNVVKLQRIEDLPTMVTLGNSFLHKLCSGFVRICMDEDGNEKRPDGVWT
 LPDQCHTVTCQPDGQTLKSHRVNCDRLRPSCPNSQSPVKVEETCGCRWTCPCVCTGS
 STRHIVTPDGNFKLTGSCSYVLFQNKQDLEVIHNGACSPGARQGCMSIEVKHSALSVE
 LHSDEMTVNGRLVSVPPYVGGNMEVNVYGAIMHEVRFNHLGHI FTFTPNNEFQLQLSPKT
 FASKTYGLCGICDENGANDFMLRDGTVTTDWKTIVQEWTVQRPQGTCQPILEEQLVPDS
 SHCQVLLPLFAECHVKLAPATFYAICQQDSCHQEQVCEVIASIAHLCRTNGVCVDWRTPD
 FCAMSCPPSLVYNHCEHGCPRHCDGNVSSCGDHPSEGCFPPDKVMLEGSCVPPEACTQ
 CIGEDGVQHGFLEAWVPDHQPCQICTCLSGRKVNCTTQPCPTAKAPTCLCEVARLRQNA
 DQCCPEYECVCDPVSDDLPPVPHCERGLQPTLTNPGECRPNFTCACRKECKRVSPSPCP
 PHRLPTLRKTQCCDEYECACNCVNSTVSCPLGYLASTATNDGCTTTTCLPDKVCVHRSTI
 YPVGQFWEEGCDVCTCTDMEDAVMGLRVAQCSQKPCEDSCRSGFTYVLHEGECCGRCL
 PSACEVVTGSPRGDSQSSWKSQVWASPENPCLINECVRVKEEVFIQQRNVSCPQLEVP
 VCPSPGFQLSCKTSACCPSCRCERMEACMLNGTVIGPGKTVMIDVCTTCRCMVQGVISGF
 KLECRKTTNCPCLGYKEENNTGECCGRCLPTACTIQLRGGQIMTLKRDETLQDGCDFHFC
 KVNERGEYFWEKRVTCPPFDEHKCLAEGGKIMKIPGTCCDTCEEPECNDITARLQYVKVG
 SCKSEVEVDIHYCQKGCASKAMYSIDINDVQDQSCCSPTRTEPMQVALHCTNGSVVYHEV
 LNAMECKCSPRKCSK

SEQ ID NO 57: amino acids 764-1242 - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser:

SLSCRPPMVKLVCADNLRAEGLECTKTCQNYDLECMGCVSGCLCPPGMVRHENRCV

ALERPCPFHQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK
 YLFPGEQYVLVQDYCGSNPGTFRILVGNKGCSHPSVKCKKRVTLVEGGEIELEFDGEVNVK
 RPMKDETHFEVVEGSGRYIILLGKALSVVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNND
 LTSSNLQVEEDPVDGNSWKVSSQCADTRKVPDLSPPATCHNNIMKQTMVDSSCRILTSV
 FQDCNKLVDPEPYLDVCIYDTCSCESIGDCACFCDTIAAYAHVCAQHGVVTVWRTATLCPQ
 SCEERNLRENGEYECWRYNSCAPACQVTCQHPEPLACPVQCVEGCHAHCPPGKILDELLQ
 TCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQ ICHCDVNNLTCEACQEPGG

SEQ ID NO 58: amino acids 764-1482 - Cysteines 1099 and 1142 are marked with bold. One or both of these cysteines can be substituted to another amino acid, e.g. Ser:

SLSCRPPMVKLVCADNLRAEGLECTKTCQNYDLECMGCVSGCLCPPGMVRHENRCV

ALERPCPFHQKEYAPGETVKIGCNTCVCQDRKWNCTDHVCDATCSTIGMAHYLTFDGLK

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YLFPGECQYVLVQDYCGSNPGTFRILVGNKGCSPSVKCKKRVTLVEGGEIELFDGEVNVK
 RPKMDETHFEVVESEGRYIILLGKALS VVWDRHLSISVVLKQTYQEKVCGLCGNFDGIQNND
 LTSSNLQVEEDPVDFGNWVSSQCADTRKVPLDSSPATCHNNIMKQTMVDSSCRILTSDV
 FQDCNKLVDPEPYLDVCIYDTCSESIGDCACFCDTIAAYAHVCAQHGVVTVWRTATLCPQ
 SCEERNLRENGYECEWRYNSCAPACQVTCQHPEPLACPVCVEGCHAHCPPGKILDELLQ
 TCVDPEDCPVCEVAGRRFASGKKVTLNPSDPEHCQICHCDVNLTCACQEPGGLVVPPT
 DAPVSPTTLYVEDISEPPLHDFYCSRLLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRISQ
 KWVRVAVVEYHDGSHAYIGLDRKRPSSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKID
 RPEASRITLLLMASQEPQRMRSNFRVYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENK
 AFVLSSVDELEQQORDEIVSYLCDLAPEAPPPTLPDMAQVTVGPGL

FVIII Molecules/Variants/Derivatives/Analogues: The term “FVIII” as used herein, is intended to designate any FVIII molecule having FVIII activity, incl. wt FVIII, B domain deleted/truncated FVIII molecules, variants of FVIII exhibiting substantially the same or improved biological activity relative to wt FVIII and FVIII-related polypeptides, in which one or more of the amino acids of the parent peptide have been chemically modified, e.g. by protein:protein fusion, alkylation, PEGylation, HESylation, PASylation, PSAylation, acylation, ester formation or amide formation or the like (conjugated to a half-life extending moiety).

Half-Life Extending Moieties/Protractive Groups: The term “half-life extending moieties” is herein understood to refer to one or more chemical groups, e.g. a hydrophilic polymer, such as e.g. PEG and/or a polysaccharide covalently attached to FVIII via e.g. —SH, —OH, —COOH, —CONH₂, —NH₂, or one or more N- and/or O-glycan structures that can increase in vivo circulatory half-life when conjugated to these proteins. Examples of protractive groups/half-life extending moieties suitable for being conjugated to FVIII in connection with the present invention include: Biocompatible fatty acids and derivatives thereof, Hydroxy Alkyl Starch (HAS) e.g. Hydroxy Ethyl Starch (HES), Poly Ethylene Glycol (PEG), Poly (Glyx-Sery)_n (HAP), Hyaluronic acid (HA), Heparosan polymers (HEP), Phosphorylcholine-based polymers (PC polymer), Fleximers, Dextran, Polysialic acids (PSA), an Fc domain, an Fc receptor, Transferrin, Albumin, Elastin like peptides, XTEN polymers, Albumin binding peptides, a CTP peptide, and any combination thereof. In general, conjugation of FVIII with one or more half-life extending moieties (such as e.g. hydrophilic polymers) generally have a better bioavailability in connection with s.c./intradermal co-administration with VWF fragments according to the invention as compared with FVIII with no half-life extending moieties.

PEGylated FVIII molecules in connection with the present invention may have one or more polyethylene glycol (PEG) molecules attached to any part of the FVIII protein including any amino acid residue or carbohydrate moiety. Chemical and/or enzymatic methods can be employed for conjugating PEG or other polymeric groups (half-life extending moieties) to a glycan on FVIII. An example of an enzymatic conjugation process is described e.g. in WO03031464. The glycan may be naturally occurring or it may be inserted via e.g. insertion of an N-linked and/or O-linked glycan using methods well known in the art. “Cysteine-PEGylated FVIII” according to the present invention have one or more PEG molecules conjugated to a sulfhydryl group of a cysteine present in FVIII. “Cysteine-acylated FVIII” according to the

present invention have one or more hydrophobic half-life extending moieties (e.g. fatty acids) conjugated to a sulfhydryl group of a cysteine in FVIII—this cysteine residue may be introduced by genetic engineering or a part of the native amino acid sequence. It is furthermore possible to link half-life extending moieties to other amino acid residues.

Fusion Proteins: Fusion proteins according to the present invention are proteins created through the in-frame joining of two or more DNA sequences which originally encoded FVIII and the fusion partner. Translation of the fusion protein DNA sequence will result in a single protein sequence which may have functional properties derived from each of the original proteins or peptides. DNA sequences encoding fusion proteins may be created artificially by standard molecular biology methods such as overlapping PCR or DNA ligation and the assembly is performed excluding the stop codon in the first 5'-end DNA sequence while retaining the stop codon in the 3' end DNA sequence. The resulting fusion protein DNA sequence may be inserted into an appropriate expression vector that supports the heterologous fusion protein expression in a standard host organism.

Fusion proteins may contain a linker or spacer peptide sequence that separates the protein or peptide parts which define the fusion protein. The linker or spacer peptide sequence may facilitate the correct folding of the individual protein or peptide parts and may make it more likely for the individual protein or peptide parts to retain their individual functional properties. Linker or spacer peptide sequences may be inserted into fusion protein DNA sequences during the in frame assembly of the individual DNA fragments that make up the complete fusion protein DNA sequence i.e. during overlapping PCR or DNA ligation. Examples of fusion proteins comprising FVIII and a fusion partner are shown in WO2011101284.

Fc Fusion Protein: The term “Fc fusion protein” is herein meant to encompass FVIII fused to an Fc domain that can be derived from any antibody isotype. An IgG Fc domain will often be preferred due to the relatively long circulatory half-life of IgG antibodies. The Fc domain may furthermore be modified in order to modulate certain effector functions such as e.g. complement binding and/or binding to certain Fc receptors. Fusion of FVIII with an Fc domain, which has the capacity to bind to FcRn receptors, will generally result in a prolonged in vivo circulatory half-life. Mutations in positions 234, 235 and 237 in an IgG Fc domain will generally result in reduced binding to the FcγRI receptor and possibly also the FcγRIIa and the FcγRIII receptors. These mutations do not alter binding to the FcRn receptor, which promotes a long circulatory in vivo half-life by an endocytic recycling path-

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way. Preferably, a modified IgG Fc domain of a fusion protein according to the invention comprises one or more of the following mutations that will result in decreased affinity to certain Fc receptors (L234A, L235E, and G237A) and in reduced C1q-mediated complement fixation (A330S and P331S), respectively. Alternatively, the Fc domain may be an IgG4 Fc domain, preferably comprising the S241P/S228P mutation.

Bioavailability (of FVIII): The term "Bioavailability" describes the percentage of compound absorbed to the blood after extravascular is calculated as the Area under the concentration time curves after extravascular dosing of the compound. This is calculated from the Area under the concentration curves of FVIII after s.c. administration divided by the dose, relatively to the area under the concentrations curve divided by the dose of the same FVIII compound, dosed i.v. According to the present invention, the bioavailability of FVIII molecules (in connection with subcutaneous/intradermal co-administration of FVIII and VWF fragments according to the invention) is at least 3%, preferably at least 5%, preferably at least 6%, preferably at least 7%, preferably at least 8%, preferably at least 9%, preferably at least 10%, preferably at least 11%, preferably at least 12%, preferably at least 13%, preferably at least 14%, preferably at least 15%, preferably at least 16%, preferably at least 17%, preferably at least 18%, preferably at least 19%, preferably at least 20%, preferably at least 21%, preferably at least 22%, preferably at least 23%, preferably at least 24%, preferably at least 25%, preferably at least 26%, preferably at least 27%, preferably at least 28%, preferably at least 29%, preferably at least 30%, preferably at least 31%, preferably at least 32%, preferably at least 33%, preferably at least 34%, preferably at least 35%, preferably at least 36%, preferably at least 37%, preferably at least 38%, preferably at least 39%, preferably at least 40%, preferably at least 41%, preferably at least 42%, preferably at least 43%, preferably at least 44%, preferably at least 45%, preferably at least 46%, preferably at least 47%, preferably at least 48%, preferably at least 49%, preferably at least 50%, preferably at least 55%, preferably at least 60%, preferably at least 65%, preferably at least 70%, and most preferably at least 75%. Bioavailability can be measured as described herein. Preferably, the FVIII bioavailability (FVIII antigen and/or activity) of formulations according to the invention will be high enough to exert prophylactic effects under conditions with normal activity when such formulations are administered extravascularly (e.g. subcutaneously or intradermally) e.g. once or twice a day or once, twice or three times a week. Preferably, FVIII dosages are comparable with those used in connection with I.V. administration of FVIII, preferably twice as high, and more preferably three times as high, more preferably four times as high, more preferably about 10 times as high, more preferably about 15 times as high, more preferably about 20 times as high, and most preferably about 25 times as high. Safety and cost considerations may be considered in connection with dosage determinations.

Saturation of FVIII with VWF Fragments according to the invention: saturation of FVIII with VWF fragment/the relative amount of FVIII bound to or in complex with VWF/the amount of FVIII bound to VWF divided by the total amount of FVIII. This calculation is based on the KD value of the binding between FVIII and the protein. For FVIII binding to VWF fragments, the measured KI values are used as KD.

The following (quadratic) equations can be used to calculate the concentration of bound FVIII (A) to another protein (B) from the total concentrations $[A]_t$, $[B]_t$.

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$$K_D = \frac{[A] \times [B]}{[AB]}$$

$$[A] = [A]_t - [AB]$$

$$[B] = [B]_t - [AB]$$

$$[AB]^2 - (K_D + [A]_t + [B]_t) \times [AB] + [A]_t \times [B]_t = 0$$

$$\alpha \times [AB]^2 + \beta \times [AB] + \delta = 0$$

$$\alpha = 1, \beta = -(K_D + [A]_t + [B]_t), \delta = [A]_t \times [B]_t$$

$$[AB] = \frac{-\beta \pm \sqrt{\beta^2 - 4 \times \alpha \times \delta}}{2 \times \alpha}$$

Pharmaceutical Compositions: The present invention provides compositions comprising VWF fragments and preferably also FVIII.

Accordingly, one object of the invention is to provide a pharmaceutical composition comprising a FVIII molecule present in a concentration from 40 IU/ml to 25,000 IU/ml, and wherein said composition has a pH from 2.0 to 10.0. In a preferred embodiment, the FVIII molecules are co-administered together with VWF fragments. In another embodiment, the pharmaceutical composition comprises (i) a FVIII molecule and (ii) a VWF fragment; in one embodiment thereof, the pharmaceutical composition is an aqueous liquid, ready-to use composition, in another embodiment, the composition is a freeze-dried composition that should be dissolved before use. Formulations of FVIII, particularly liquid formulations, are stabilised against degradation by addition of VWF fragments. Pharmaceutical compositions according to the invention may thus comprise FVIII in a concentration of from 40 IU/ml to 25,000 IU/ml, such as e.g. from 50-25,000 IU/ml, 100-25,000 IU/ml, 250-25,000 IU/ml, 500-25,000 IU/ml, 1000-25,000 IU/ml, 2000-25,000 IU/ml, 3000-25,000 IU/ml, 4000-25,000 IU/ml, 5000-25,000 IU/ml, 6000-25,000 IU/ml, 7000-25,000 IU/ml, 8000-25,000 IU/ml, 9000-25,000 IU/ml, 10,000-25,000 IU/ml, 50-20,000 IU/ml, 100-20,000 IU/ml, 250-20,000 IU/ml, 500-20,000 IU/ml, 1000-20,000 IU/ml, 2000-20,000 IU/ml, 3000-20,000 IU/ml, 4000-20,000 IU/ml, 5000-20,000 IU/ml, 6000-20,000 IU/ml, 7000-20,000 IU/ml, 8000-20,000 IU/ml, 9000-20,000 IU/ml, 10,000-20,000 IU/ml, 50-15,000 IU/ml, 100-15,000 IU/ml, 250-15,000 IU/ml, 500-15,000 IU/ml, 1000-15,000 IU/ml, 2000-15,000 IU/ml, 3000-15,000 IU/ml, 4000-15,000 IU/ml, 5000-15,000 IU/ml, 6000-15,000 IU/ml, 7000-15,000 IU/ml, 8000-15,000 IU/ml, 9000-15,000 IU/ml, 10,000-15,000 IU/ml, 50-10,000 IU/ml, 100-10,000 IU/ml, 250-10,000 IU/ml, 500-10,000 IU/ml, 1000-10,000 IU/ml, 2000-10,000 IU/ml, 3000-10,000 IU/ml, 4000-10,000 IU/ml, 5000-10,000 IU/ml, 50-5000 IU/ml, 100-5000 IU/ml, 250-5000 IU/ml, 500-5000 IU/ml, and 1000-5000 IU/ml. Compositions according to the invention may further comprise one or more pharmaceutically acceptable excipients such as e.g. a buffer system, a preservative, a tonicity agent, a chelating agent, a stabilizer, or a surfactant, as well as various combinations thereof. The use of preservatives, isotonic agents, chelating agents, stabilizers and surfactants in pharmaceutical compositions is well-known to the skilled person. Reference may be made to Remington: The Science and Practice of Pharmacy, 19th edition, 1995.

In one embodiment, the pharmaceutical composition is an aqueous composition. Such a composition is typically a solution or a suspension, but may also include colloids, dispersions, emulsions, and multi-phase materials. The term "aqueous composition" is defined as a composition comprising at least 50% w/w water. Likewise, the term "aqueous solution"

is defined as a solution comprising at least 50% w/w water, and the term "aqueous suspension" is defined as a suspension comprising at least 50% w/w water. In one embodiment, the pharmaceutical composition is an aqueous solution; in another embodiment it is a liquid, ready-to-use composition. 5

In another embodiment, the pharmaceutical composition is a freeze-dried composition, to which the physician or the patient adds solvents and/or diluents prior to use.

In one embodiment, the pharmaceutical compositions according to the present invention are suitable for extravascular administration (e.g. s.c. or intradermal administration) in prophylactic/therapeutic treatment of blood clotting diseases. In another embodiment, the pharmaceutical composition is suitable for intravenous administration. 10

In one embodiment, the pharmaceutical composition according to the invention is a pharmaceutical composition for intravenous administration; in further embodiments thereof, the pharmaceutical composition is (i) a freeze-dried composition or (ii) a liquid composition. 15

"Ratio of FVIII:VWF": According to the present invention, preferred ratios of FVIII and VWF/VWF fragment include FVIII/VWF ratios (molar ratios) from 0.5:1 to 1:50, such as e.g. 1:1 to 1:50, such as e.g. 1:1 to 1:25, such as e.g. 1:1 to 1:20, or 1:1 to 1:15, or 1:1 to 1:10, or 1:1 to 1:7.5, or 1:7 to 1:8, or 1:6 to 1:8, or 1:6 to 1:9, or 1:5 to 1:10. Preferred ratios thus include: 1:1, 1:2, 1:3, 1:4, 1:5, 1:5.5, 1:6, 1:6.5, 1:7, 1:7.1, 1:7.2, 1:7.3, 1:7.4, 1:7.5, 1:7.6, 1:7.7, 1:7.8, 1:7.9, 1:8, 1:9, 1:10, 1:15, 1:20, 1:25, 1:30, 1:35, 1:40, 1:45, and 1:50. Preferred ratios include: 0.5:1, 0.6:1, 0.7:1, 0.8:1, 0.9:1, 1:1, 1.1:1, 1.2:1, 1.3:1, 1.4:1, and 1.5:1. A molar ratio close to 1:1 generally has the advantage of minimizing the required amount of active substance. The optimal ratio between FVIII and VWF fragment in a co-formulation mixture may be determined by calculating the amount of bound FVIII:VWF at certain protein concentrations based on the binding affinity to the VWF variant for the FVIII species in question. The binding affinity can be determined e.g. by ELISA, SPR or by ITC. 20 25 30 35

"Haemophilia": Haemophilia/hemophilia/blood clotting diseases is a group of hereditary genetic disorders that impair the body's ability to control blood clotting or coagulation ("bleeding disorders"), which is used to stop bleeding when a blood vessel is broken. Haemophilia A (clotting factor VIII deficiency) is the most common form of the disorder, present in about 1 in 5,000-10,000 male births. In connection with the present invention, the term "haemophilia" encompasses von Willebrand disease. 40 45

List of Embodiments:

1. A VWF fragment comprising up to 1500, 1400, 1300, or 1200, wherein said VWF fragment comprises the TIL' domain. Said fragment may comprise different or repetitive VWF sequences joined by peptide bonds. 50
2. A VWF fragment according to the invention, wherein said fragment comprises the TIL' and the E' domains.
3. A VWF fragment consisting of the TIL' or the TIL'/E' domains. 55
4. A VWF fragment (according to the invention), wherein said fragment comprises the amino acid sequence according to any one of SEQ ID NO 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 57 or 58.
5. A VWF fragment according to the invention, wherein said VWF fragment does not comprise cysteine residues at position(-s) 1099 and/or 1142 of SEQ ID NO 22. These cysteine residue(-s) can be deleted by amino acid substitution and/or deletion. 60
6. A VWF fragment according to the invention, wherein said fragment comprises SEQ ID NO 9, wherein the 1099 Cysteine residue is substituted with another amino 65

acid, such as e.g. Histidine, Alanine, Isoleucine Arginine, Leucine, Asparagine, Lysine, Aspartic acid, Methionine, Phenylalanine, Glutamic acid, Threonine, Glutamine, Tryptophan, Glycine, Valine, Proline, Serine, Taurine, and Tyrosine.

7. A VWF fragment according to the invention, wherein the 1099 cysteine residue is substituted with Serine.
8. A VWF fragment according to the invention, wherein said fragment comprises an amino acid sequence selected from the list consisting of: SEQ ID NO 10, SEQ ID NO 11, SEQ ID NO 12, SEQ ID NO 13, SEQ ID NO 14, SEQ ID NO 15, SEQ ID NO 16, SEQ ID NO 17, SEQ ID NO 18, SEQ ID NO 19, SEQ ID NO 20, SEQ ID NO 21, SEQ ID NO 57 and SEQ ID NO 58 wherein the 1099 and the 1142 cysteine residues are substituted with another amino acid, such as e.g. Histidine, Alanine, Isoleucine Arginine, Leucine, Asparagine, Lysine, Aspartic acid, Methionine, Phenylalanine, Glutamic acid, Threonine, Glutamine, Tryptophan, Glycine, Valine, Proline, Serine, Taurine, and/or Tyrosine.
9. A VWF fragment according to the invention, wherein the 1099 and the 1142 cysteine residues are substituted with serine.
10. A pharmaceutical composition comprising a VWF fragment according to the invention, wherein less than 10%, preferably less than 9%, preferably less than 8%, preferably less than 7%, preferably less than 6%, preferably less than 5%, preferably less than 4%, preferably less than 3%, preferably less than 2%, preferably less than 1% of said VWF fragment are in the form of oligomers and/or multimers.
11. A VWF fragment according to the invention, wherein said VWF fragment is part of a dimer. The percentage of dimer formation may be at least 5%, preferably at least 10%, preferably at least 15%, preferably at least 20%, preferably at least 25%, preferably at least 30%, preferably at least 35%, preferably at least 40%, preferably at least 45%, preferably at least 50%, preferably at least 55%, preferably at least 60%, preferably at least 65%, preferably at least 70%, preferably at least 75%, preferably at least 80%, preferably at least 85%, preferably at least 90%, most preferably at least 95%.
12. A pharmaceutical composition comprising FVIII and a VWF fragment, wherein FVIII bioavailability is at least 5% following extravascular (e.g. sub-cutaneous/intradermal) administration of said pharmaceutical formulation.
13. A pharmaceutical composition comprising FVIII and a VWF fragment, wherein FVIII bioavailability is at least 5% following extravascular (e.g. sub-cutaneous/intradermal) administration of said pharmaceutical formulation, wherein the ratio of FVIII and VWF fragment is about 0.5:1-1:50. Preferably said ratio is about 0.5:1, 1:1, or 1:2.
14. A VWF fragment, wherein the amino acid sequence of said VWF fragment comprises or consists of an amino acid sequence selected from the list consisting of: SEQ ID NO 4, SEQ ID NO 5, SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 8, SEQ ID NO 9, SEQ ID NO 10, SEQ ID NO 11, SEQ ID NO 12, SEQ ID NO 13, SEQ ID NO 14, SEQ ID NO 15, SEQ ID NO 16, SEQ ID NO 17, SEQ ID NO 18, SEQ ID NO 19, SEQ ID NO 20, SEQ ID NO 21, SEQ ID NO 57 and SEQ ID NO 58.
15. A pharmaceutical composition comprising: (i) a VWF fragment according to the invention; and (ii) FVIII, preferably recombinant FVIII. Alternatively, said composition may comprise two, three, four, five or more different

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- VWF fragments according to the invention and/or two, three, four, or five different FVIII molecules.
16. A pharmaceutical composition according to the invention, wherein said FVIII molecule comprises a truncated B domain at a size of 5-700 amino acids, such as e.g. 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, 5-40, 5-30, 5-25, 5-20, 10-700, 10-500, 10-400, 10-300, 10-200, 10-100, 10-50, 10-40, 10-30, 10-20, 20-700, 20-500, 20-400, 20-300, 20-200, 20-100, 20-50, 20-25, 50-700, 50-500, 50-400, 50-300, 50-200, 50-100, 100-700, 100-500, 100-400, 100-300, 100-200, 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 75, or 100 amino acids
 17. A pharmaceutical composition according to the invention, wherein the amino acid sequence of said truncated B domain is derived from the wt FVIII B domain amino acid sequence.
 18. A pharmaceutical composition according to the invention, wherein said FVIII molecule is a B domain truncated FVIII molecule, wherein said B domain comprises an O-glycan linked to the Ser 750 amino acid residue as set forth in SEQ ID NO 1. Preferably, said FVIII molecule comprises one O-linked glycan in the truncated B domain, wherein said O-linked glycan is attached to the Ser 750 residue as set forth in SEQ ID NO 1.
 19. A pharmaceutical composition according to the invention, wherein said FVIII molecule comprises a B domain having the amino acid sequence as set forth in SEQ ID NO 2. Alternatively, one or more amino acids in the B domain are deleted from SEQ ID NO 2, such as e.g. the N-terminal Ser residue and/or the C-terminal Arg residue.
 20. A pharmaceutical composition according to the invention, wherein the amino acid sequence of the FVIII B domain comprises or consists of an amino acid sequence selected from the group consisting of: amino acids 741-857+1637-1648; amino acids 741-914+1637-1648; amino acids 741-954+1637-1648; amino acids 741-965+1637-1648; amino acids 741-965+1637-1648; amino acids 741-1003+1637-1648; amino acids 741-1003+1637-1648; amino acids 741-1020+1637-1648; amino acids 741-1079+1637-1648; amino acids 741-1206+1637-1648; amino acids 741-1261+1637-1648; amino acids 741-1309+1637-1648; amino acids 741-914+1637-1648; amino acids 741-954+1637-1648; amino acids 741-968+1637-1648; amino acids 741-1003+1637-1648; amino acids 741-1018+1637-1648; amino acids 741-1070+1637-1648; amino acids 741-1230+1637-1648; amino acids 741-1301+1637-1648; amino acids 741-965+1637-1648; amino acids 741-965+1637-1648; and amino acids 741-965+1637-1648 as set forth in SEQ ID NO 1.
 21. A pharmaceutical composition according to the invention, wherein said FVIII molecule is conjugated with at least one half-life extending moiety. Preferably, said half-life extending moiety is a water soluble polymer. Preferably a PEG and/or a polysaccharide.
 22. A pharmaceutical composition according to the invention, wherein at least one water soluble polymer is covalently attached to a glycan present in the B domain, preferably an O-glycan, preferably an O-glycan attached to the Ser750 amino acid residue as set forth in SEQ ID NO 1.

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23. A pharmaceutical composition according to the invention, wherein said water soluble polymer is selected from the group consisting of: PEG, PSA, HES, HEP and HSA.
24. A pharmaceutical composition according to the invention, wherein said FVIII molecule is produced using an expression vector encoding a FVIII molecule comprising the FVIII B domain is as set forth in SEQ ID NO 2.
25. A pharmaceutical composition according to the invention, wherein the bioavailability of said FVIII molecule is at least 2, 3, 4, 5, 6, 7, 8, 9, or 10%. Preferably, the bioavailability is measured as the area under the curve of the plasma levels of FVIII after subcutaneous administration using either an antigen assay or a clotting assay.
26. A pharmaceutical composition according to the invention, wherein the ratio between FVIII and VWF is 1:50, 1:34, 1:25, 1:20:1:15, 1:10:1:7.5, preferably 0.5:1, 1:1, or 1:2.
27. A pharmaceutical formulation according to the invention, wherein the concentration of FVIII is at least about 100, 150, 200, 250, 300, 350, 400, 500, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000, or 30,000 IU/ml.
28. A pharmaceutical formulation according to the invention, wherein the amount of FVIII bound to VWF fragment is at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, or 95% of the total amount of FVIII in said formulation.
29. Use of a compound according to the invention, or a pharmaceutical composition according to the invention, for treatment of haemophilia by extravascular, preferably subcutaneous, administration. The pharmaceutical composition according to the invention can also be administered by intradermal administration. The pharmaceutical composition according to the invention can furthermore be administered by intravenous administration.
30. A method of treatment of a haemophilia, wherein said method comprises subcutaneous administration of a therapeutically effective amount of a compound according to the present invention, or a pharmaceutical composition according to the present invention, to a patient in need thereof.
31. A method of increasing bioavailability of FVIII, wherein said method comprises a step of extravascular (e.g. subcutaneous/intradermal) co-administration of FVIII and a VWF fragment according to the invention, wherein the ratio of said FVIII and said VWF fragment is about 1:1-1:50, preferably 0.5:1, 1:1, 1:2, 1:10, 1:20 or 1:34.
32. A DNA molecule encoding a VWF fragment according to the invention.
33. An expression vector comprising a DNA molecule according to the invention.
34. A host cell comprising an expression vector according to the invention.
35. A method for making a VWF fragment according to the invention, wherein said method comprises incubation of a host cell in a suitable medium under suitable conditions and subsequently recovering said recombinant VWF fragment.
36. A pharmaceutical composition according to the invention, wherein said composition comprises one or more VWF fragments according to the invention.

37. A pharmaceutical composition comprising one or more VWF fragments according to the invention.
 38. A method of treatment of von willebrand disease, wherein said method comprises extravascular (e.g. subcutaneous) administration of a therapeutically effective amount of a pharmaceutical composition according to the present invention, to a patient in need thereof.
 39. A VWF fragment or VWF-like polypeptide comprising the 15 N terminal amino acids of the TIL' sequence 764-778, or more.
 40. A VWF fragment according to the invention, wherein said VWF fragment interacts with/binds to residues C1858-Q1874, S2063-D2074 AND V2125-A2146 of the FVIII amino acid sequence as set forth in SEQ ID NO 1.
 41. A VWF fragment according to the invention, wherein said fragment is conjugated with a half-life extending moiety.
 42. A VWF fragment according to the invention, wherein said fragment is conjugated with a half-life extending moiety via a N- and/or O-linked glycan.
 43. A VWF fragment according to the invention, wherein said VWF fragment reduced uptake of FVIII by antigen presenting cells in connection with binding of said VWF fragment to FVIII.
 44. A pharmaceutical composition according to the invention, wherein the pharmaceutical composition is for intravenous administration.
 45. A pharmaceutical composition according to the invention, which is a freeze-dried composition.
 46. A pharmaceutical composition according to the invention, which is a liquid composition.
 47. A pharmaceutical composition according to the invention, wherein the pharmaceutical composition is for intravenous administration and is a freeze-dried composition.
 48. A pharmaceutical composition according to the invention, wherein the pharmaceutical composition is for intravenous administration and is a liquid composition.
- It is understood that all aspects and embodiments of the invention can be combined and that they are not to be understood in any limiting way.

EXAMPLES

While certain features of the invention have been illustrated and described herein, many modifications, substitutions, changes, and equivalents will now occur to those of ordinary skill in the art. It is, therefore, to be understood that the appended claims are intended to cover all such modifications and changes as fall within the true spirit of the invention.

Example 1

Subcutaneous Administration in FVIII Knockout Mice (1): Two test compounds were prepared:

- a) GlycoPEGylated FVIII, i.e. "N8-GP" (prepared essentially as disclosed in example 1+2 in WO2009108806) 2000 U FVIII/ml determined by chromogenic activity equivalent to 1.2 μ M based on protein content.
- b) GlycoPEGylated FVIII i.e. N8-GP (2000 U FVIII/ml or 1.2 μ M, co-formulated with 0.74 mg/ml VWF fragment TIL'/E'/D3/A1 (equivalent to 9.3 μ M) Both test compounds were formulated in 18 mg/ml NaCl, 3 mg/ml saccharose, 1.5 mg/ml L-histidine, 0.1 mg/ml polysorbate 80, 0.25 mg/ml CaCl₂, pH 7.3

12 FVIII KO mice, exon 16 knock-out in a mixed background of C57Bl/6 and SV129, bred at Taconic M&B (B6.129S4-F8tm1Kaz/J) with an approximate weight of 22 g were dosed subcutaneously in the flank with 10000 IU/kg FVIII or FVIII/VWF, 6 mice with each test compound.

Blood was sampled at 1, 3, 7, 17, 24, 30, 48, 72 and 96 h post administration. The mice were anaesthetized by Isoflurane/O₂/N₂O prior to blood sampling via the retroorbital plexus. Three samples were taken from each mouse. Blood (45 μ l) was stabilised with 5 μ l of sodium-citrate (0.13 M) and added 200 μ l FVIII coatest SP buffer (50 mM TRIS-HCl, 1% BSA, Ciprofloxacin 10 mg/L, pH 7.3). After centrifugation at 4000 g for 5 minutes at room temperature, the supernatants were immediately frozen on dry ice before storage at -80° C. prior to analysis.

Samples were analysed with regards to FVIII activity in a chromogenic assay as described by Ovlisen K et al. J. Thromb. Haemost, 2008, 6: 969-975 and by FVIII antigen analysis using two FVIII light chain antibodies (4F45 and 4F11) in a FVIII LOCI assay (Luminescence oxygen channelling immunoassay).

Mean plasma concentration versus time data were analysed by non-compartmental analysis using WinNonlin Phoenix (Pharsight Corporation) estimating the given pharmacokinetic parameters. The bioavailability was estimated using a previous i.v. pharmacokinetic study of N8-GP in FVIII KO mice.

The circulating profiles of FVIII activity are shown graphically in FIG. 1, the circulating concentrations of FVIII antigen are shown in FIG. 2.

In this experiment, the bioavailability of GlycoPEGylated FVIII alone was calculated to be 27% based on activity and 19% based on antigen. The co-formulation with VWF increased the bioavailability to 40 and 47%, respectively.

Example 2

Subcutaneous Administration in FVIII Knockout Mice (2): Two test compounds were prepared:

- a) GlycoPEGylated FVIII (500 IU FVIII/ml determined by chromogenic activity equivalent to 0.3 μ M)
- b) GlycoPEGylated FVIII (500 IU FVIII/ml or 0.3 μ M, co-formulated with 0.185 mg/ml VWF fragment TIL'/E'/D3/A1 (equivalent to 2.3 μ M)

Based on a measured IC₅₀ of 1.5 nM of the VWF fragment to FVIII and assuming that the measured IC₅₀ equals K_d, 99% of the FVIII should be bound to VWF in this composition.

Both test compounds were formulated in 18 mg/ml NaCl, 3 mg/ml saccharose, 1.5 mg/ml L-histidine, 0.1 mg/ml polysorbate 80, 0.25 mg/ml CaCl₂, pH ~7.3

12 FVIII KO mice, exon 16 knock-out in a mixed background of C57Bl/6 and SV129, bred at Taconic M&B (B6.129S4-F8tm1Kaz/J) with an approximate weight of 22 g were dosed subcutaneously in the flank with 2500 IU/kg FVIII or FVIII/VWF, 6 mice with each test compound.

Blood was sampled at 1, 3, 7, 17, 24, 30, 48, 72 and 96 h post administration. The mice were anaesthetized by Isoflurane/O₂/N₂O prior to blood sampling via the retroorbital plexus. Three samples were taken from each mouse. 45 μ l of blood was stabilised with 5 μ l of sodium-citrate (0.13 M) and added 200 μ l FVIII coatest SP buffer (50 mM TRIS-HCl, 1% BSA, Ciprofloxacin 10 mg/L, pH 7.3). After centrifugation at 4000 g for 5 minutes at room temperature, the samples were immediately frozen on dry ice before storage at -80° C. prior to analysis.

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Samples were analysed with regards to FVIII activity in a chromogenic assay as described by Ovlisen K et al. J. Thromb. Haemost, 2008, 6: 969-975 and by FVIII antigen analysis using two FVIII light chain antibodies (4F45 and 4F11) in a FVIII LOCI assay (Luminescence oxygen channeling immunoassay).

Mean plasma concentration versus time data were analysed by non-compartmental analysis using WinNonlin Phoenix (Pharsight Corporation) estimating the given pharmacokinetic parameters. The bioavailability was estimated using a previous i.v. pharmacokinetic study of N8-GP in FVIII KO mice.

The circulating profiles of FVIII activity are shown graphically in FIG. 3, the circulating concentrations of FVIII antigen are shown in FIG. 4.

In this experiment, the bioavailability of GlycoPEGylated FVIII alone was calculated to be 29% based on activity and 14% based on antigen. The co-formulation with VWF increased the bioavailability to 36% (antigen measurement).

Example 3

Haemostatic Efficacy of s.c. Administered Co-Formulations of FVIII Compounds with VWF Compounds:

Study Outline:

Animals: FVIII k/o mice, 8-18 weeks old, male and females

Tail bleeding: n=6-12 per timepoint/group

Thrombo-elastography: n=2-4 per timepoint/group

Administration route: s.c. in the neck or flank (i.v. in the tail vein for control groups)

Dose volumes 1-10 ml/kg

Groups:

Vehicle controls dosed 24 hr prior to injury

i.v. controls dosed 5 min prior to injury

FVIII compounds co-formulated with VWF compounds dosed s.c. 5 min, 1, 3, 5, 12, 24, 48, 72, 96, 120, 144 or 168 hr prior to injury.

Procedures:

Compounds of interest are prepared in buffer (10 mM L-Histidine, 8.8 mM Sucrose, 0.01% Polysorbate 80, 308 mM NaCl, 1.7 mM CaCl₂ (dihydrate), 0.37 mM L-Methionine, pH 6.9) to a concentration between 40 and 10000 U/ml and stored at -80 C until use.

Before tail transection, the mice are anaesthetised with isoflurane and placed on a heating pad

The tails are placed in pre-heated saline at 37° C. for 10 min

I.v. controls are injected 5 min, 24 or 48 hr prior to injury

The tail is transected 4 mm from the tip

Immediately before tail cut a 20 µl blood sample is drawn from the peri-orbital plexus for FVIII determination

Blood is collected over 30 min and the haemoglobin concentration determined by spectrophotometry at 550 nm

Parallel animals are used for blood sampling and subsequent analysis of their clotting parameters (ex vivo efficacy).

Results:

The prophylactic effect of the co-formulation is determined from comparing the blood loss during the 30 min study period at a certain time after s.c. administration (5 min until 168 hr) to that of 1, a vehicle control and 2, an i.v. control group with FVIII or glycoPEGylated FVIII. FIG. 10 shows that glycoPEGylated FVIII are haemostatic effective 24 hr after s.c. administration of 2500 U/kg as shown by reduction of blood loss and shortening of clot time ex vivo. Similar effect is seen for FVIII co-formulated with a VWF fragment.

Example 4

Evaluation of Bioavailability of FVIII:

Bioavailability of co-compositions of FVIII and VWF/VWF fragments according to the invention can be determined

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from evaluations of the effect on bioavailability in PK experiments as those described in examples 1 and 2 as well as evaluations of the prophylactic effect as described in example 3.

The bioavailability of a FVIII compound co-formulated with a concentration of VWF fragment that enables the majority of FVIII to be bound to a VWF fragment compound in the injection composition can be determined from the concentration of FVIII compound in the composition and from experiments evaluating the binding affinity of the VWF fragment compound to the FVIII compound such as e.g. surface plasmon resonance experiments.

Example 5

Titration of Dosis of FVIII: VWF Co-Composition:

Dose titration can be carried out as disclosed in examples 1-3. Briefly, plasma concentration of FVIII will be evaluated after s.c. administration of doses of 70, 100, 150, 280, 500, 1000 and 2500 IU/kg (FVIII units) alone or together with a VWF fragment in FVIII k/o mice.

Example 6

Titration of Ratio Between FVIII Compound and VWF Compound:

Titration of ratios between FVIII and VWF can be carried out as disclosed in experiments similar to that in examples 1 and 2 as well as that described in example 3.

For PK evaluation, doses of 280, 500, 1000 or 2500 IU/kg FVIII compound will be co-formulated with VWF fragments at a molar ratio of 1:1, 1:1.5, 1:2, 1:3, 1:4, 1:5, 1:7.7 or up to 1:100 (FVIII to VWF fragment) and plasma concentration of FVIII evaluated in FVIII k/o mice after s.c. administration. The maximum molar surplus of VWF fragment to FVIII will be determined from binding affinities of the fragment to the FVIII compound in question; the highest molar surplus used will be the one that should result in at least 99% of the FVIII used bound to a VWF fragment.

For prophylactic effect, the candidate compositions from the PK experiments will be evaluated in efficacy models, such as the tail bleeding described in example 3.

Example 7

Effect of VWF on Immunogenicity of FVIII

The immuno-modulatory effect of VWF co-formulated with a FVIII compound is evaluated in comparison to wild type FVIII and FVIII compounds alone.

In vivo, the relative immunogenicity is evaluated from the titer of FVIII binding antibodies and the determination of the level of neutralizing antibodies (inhibitors) at certain time points after administration. The assay for detection of FVIII binding antibodies is a radioimmunoassay (RIA). Briefly, anti-FVIII antibodies from a sample bind to radioactive ¹²⁵I-labelled rFVIII. Immunoglobulin and immune complexes bind to protein G-sepharose and is precipitated by centrifugation. The radioactivity in the precipitate is measured and this is proportional to the amount of anti-FVIII antibodies in the sample. The result is expressed in percent of the total amount of added radioactivity. i.e. as % bound/total (% B/T).

Samples positive for anti-FVIII antibodies are analysed for the presence of FVIII neutralizing antibodies using a chromogenic assay. Briefly, samples are incubated with 1 IU/ml FVIII for 1 hr. The remaining FVIII activity is determined by addition of FIX, FX, thrombin, CaCl₂ and phospholipids. After incubation the amount of generated FXa is determined

by addition of the chromogenic substrate S-2760 and the change in optical density (OD) is measured. The OD change is proportional to FVIII activity in the samples, and is compared to samples containing a known amount of FVIII and no inhibitors. The % remaining activity of the test sample is calculated compared to the reference samples without inhibitors/anti-FVIII antibodies added. Furthermore, the presence of anti-VWF antibodies is measured by ELISA using monoclonal or polyclonal anti-human VWF antibodies which does not cross react with murine VWF. If a strong anti-VWF response is detected, this can be expected to interfere with the binding of VWF to FVIII and the *in vivo* analysis is repeated using murine VWF fragments.

The appearance of anti-drug antibodies is evaluated after repeated (e.g. once weekly for 4 weeks or once daily for three weeks) s.c. administration of the compounds in naïve mice, in FVIII k/o mice as well as in mice tolerized to human FVIII. The readout is the ratio of animals with positive titres at certain time points after the first and/or the last administration (e.g. 1, 2, 3, 4, 5, 6, 7 or 8 weeks). FVIII k/o mice are injected weekly e.g. with 1000 IU/kg FVIII alone or in combination with VWF in a molar ratio ensuring that at least e.g. 87% of FVIII is bound to VWF. For daily administration, the FVIII dose is lower and based upon the bioavailability of the FVIII-VWF complex. Mice tolerized to hFVIII are injected weekly for e.g. eight weeks s.c. with e.g. 1000 IU/kg FVIII with or without VWF and in some experiments including additional challenge with complete Freund's adjuvant (CFA) for the first injection followed by weekly challenges by incomplete Freund's adjuvant (IFA).

Relative immunogenicity of VWF versus VWF fragments and of wild type FVIII versus a FVIII compound co-formulated with VWF is furthermore evaluated *in vitro* in a human CD4+ T-cell assay. This is done using peripheral blood mononuclear cells (PBMCs) depleted of CD8+ T-cells. FVIII is added to the cell culture e.g. for eight days. T-cell proliferation is evaluated during the course of the assay by pulsing for e.g. 18 h with ³H-thymidine in sub-samples from the cultures and subsequently measuring ³H-thymidine incorporation. Interleukin 2 production is measured at the end of the assay using an ELISPOT IL-2 kit e.g. from R&D Systems, following the manufacturer's instructions. The data obtained in the assays are converted to a "stimulation index" describing the ratio between compound-stimulated versus un-stimulated cells.

The HLA-binding capacity of VWF has been evaluated using *in silico* analysis of HLA-binding properties. Strong binding to a sequence in a modified VWF may indicate novel T-cell epitopes, although the *in silico* analysis tool is predicting epitopes that may not be processed by the naturally occurring proteases. In order to predict if the Cys->Ser mutation will induce a risk of induced immunogenicity in the VWF-mutants, the VWF protein sequences are applied to an *in silico* peptide/HLA-II binding prediction software. The peptide/HLA-II binding prediction software is based on two different algorithms, NetMHCIIpan 2.1 (NetMHCIIpan-2.0—Improved pan-specific HLA-DR predictions using a novel concurrent alignment and weight optimization training procedure. Nielsen M, Lundegaard C, Justesen S, Lund O, and Buus S. Immunome Res. 2010 Nov. 13; 6(1):9) performing pan-specific HLA-DR predictions—and NetMHCII 2.0 (NN-align—A neural network-based alignment algorithm for MHC class II peptide binding prediction. Nielsen M and Lund O. BMC Bioinformatics. 2009 Sep. 18; 10:296) performing HLA-DP/DQ predictions.

Twenty-three amino acid long peptides with the point of mutation in position 12 are used as input to the algorithms.

The optimal processed peptide is assumed to be a 15'mer peptide with a nine amino acid core peptide binding to the HLA-II. The output is 15 amino acid long peptides with 9 amino acid long core peptides (in contact with HLA-II) and the predicted binding affinities in nanomolar.

The predicted binding affinities of the VWF mutant peptides are in the same range as the binding affinities of the wild type sequences (data not shown)—and because the peptides are predicted to bind with relatively poor affinity to the HLA-II molecules, the risk of inducing novel CD4+ T-cell epitopes is considered to be very low.

Of note, the *in silico* peptide/HLA-II binding predictions are based on experimental peptide/HLA-II binding data where it is very challenging to test cysteine-rich peptides (due to the nature of the peptides). Thus, cysteine-rich peptides are underrepresented in data sets used to train the different prediction algorithms. Therefore, the peptide/HLA-II binding predictions of these cysteine-rich VWF peptides are uncertain and should be analysed further using other immunogenicity prediction platforms (etc. *in vitro* peptide/HLA-II binding assays or *ex vivo* T-cell assays).

Example 8

Subcutaneous Administration in FVIII Knockout Mice (3):
Two Test Compounds were Prepared:

- B-domain truncated FVIII ("turoctocog alfa"/"N8"—produced essentially as disclosed in example 1 in WO2009108806) (4000 IU FVIII/ml determined by chromogenic activity assay and equivalent to 2.4 µM)
- B-domain truncated FVIII (turoctocog alfa) (1000 IU FVIII/ml determined by chromogenic activity assay and equivalent to 0.6 µM) co-formulated with 0.37 mg/ml VWF fragment TIL'E/D3/A1 (equivalent to 4.6 µM)

Based on a measured binding affinity of 1.5 nM of the VWF fragment to FVIII, 99% of the FVIII should be bound to VWF in this composition.

Both test compounds were formulated in 18 mg/ml NaCl, 3 mg/ml saccharose, 1.5 mg/ml L-histidine, 0.1 mg/ml polysorbate 80, 0.25 mg/ml CaCl₂, pH ~7.3

12 FVIII KO mice, exon 16 knock-out in a mixed background of C57Bl/6 and SV129, bred at Taconic M&B (B6.129S4-F8tm1Kaz/J) with an approximate weight of 22 g were dosed subcutaneously in the flank with 10000 IU/kg FVIII or FVIII/VWF, 6 mice with each test compound.

Blood was sampled at 1, 3, 7, 17, 24, 30, 48, 72 and 96 h post administration. The mice were anaesthetized by Isoflurane/O₂/N₂O prior to blood sampling via the retroorbital plexus. Three samples were taken from each mouse. 45 µl of blood was stabilised with 5 µl of sodium-citrate (0.13 M) and added 200 µl FVIII coatest SP buffer (50 mM TRIS-HCl, 1% BSA, Ciprofloxacin 10 mg/L, pH 7.3). After centrifugation at 4000 g for 5 minutes at room temperature, the supernatants were immediately frozen on dry ice before storage at -80° C. prior to analysis.

Samples were analysed with regards to FVIII activity in a chromogenic assay as described by Ovlisen K et al. J. Thromb. Haemost, 2008, 6: 969-975 and by FVIII antigen analysis using two FVIII light chain antibodies (4F45 and 4F11) in a FVIII LOCI assay (Luminescence oxygen channeling immunoassay).

Mean plasma concentration versus time data were analysed by non-compartmental analysis using WinNonlin Phoenix (Pharsight Corporation) estimating the given pharmacokinetic parameters.

kinetic parameters. The bioavailability was estimated using a previous i.v. pharmacokinetic study of N8-GP in FVIII KO mice.

The circulating profiles of FVIII activity are shown graphically in FIG. 5 and antigen levels are shown in FIG. 6.

In this experiment, the bioavailability of B-domain truncated FVIII alone was calculated to be 0.9% based on activity. The co-formulation with the VWF fragment increased the bioavailability to 11%.

Example 9

Subcutaneous Administration in FVIII Knockout Mice (4):
Two Test Compounds were Prepared:

- a) 226 amino acid B domain variant (1000 IU FVIII/ml determined by chromogenic activity assay and equivalent to 2.4 μ M)
- b) 226 amino acid B domain variant (1000 IU FVIII/ml determined by chromogenic activity assay and equivalent to 0.6 μ M) co-formulated with 0.37 mg/ml VWF fragment TIL/E/D3/A1 (equivalent to 4.6 μ M)

Based on a measured binding affinity of 1.5 nM of the VWF fragment to FVIII, 99% of the FVIII should be bound to VWF in this composition.

Both test compounds were formulated in 18 mg/ml NaCl, 3 mg/ml saccharose, 1.5 mg/ml L-histidine, 0.1 mg/ml polysorbate 80, 0.25 mg/ml CaCl₂, pH ~7.3

12 FVIII KO mice, exon 16 knock-out in a mixed background of C57Bl/6 and SV129, bred at Taconic M&B (B6.129S4-F8tm1Kaz/J) with an approximate weight of 22 g were dosed subcutaneously in the flank with 10000 IU/kg FVIII or FVIII/VWF, 6 mice with each test compound.

Blood was sampled at 1, 3, 7, 17, 24, 30, 48, 72 and 96 h post administration. The mice were anaesthetized by Isoflurane/O₂/N₂O prior to blood sampling via the retro-orbital plexus. Three samples were taken from each mouse. 45 μ l of blood was stabilised with 5 μ l of sodium-citrate (0.13 M) and added 200 μ l FVIII coatest SP buffer (50 mM TRIS-HCl, 1% BSA, Ciprofloxacin 10 mg/L, pH 7.3). After centrifugation at 4000 g for 5 minutes at room temperature, the supernatants were immediately frozen on dry ice before storage at -80° C. prior to analysis.

Samples were analysed with regards to FVIII activity in a chromogenic assay as described by Ovlisen K et al. J. Thromb. Haemost, 2008, 6: 969-975 and by FVIII antigen analysis using two FVIII light chain antibodies (4F45 and 4F11) in a FVIII LOCI assay (Luminescence oxygen channelling immunoassay).

Mean plasma concentration versus time data were analysed by non-compartmental analysis using WinNonlin Phonix (Pharsight Corporation) estimating the given pharmacokinetic parameters. The bioavailability was estimated using a previous i.v. pharmacokinetic study of N8-GP in FVIII KO mice.

In this experiment, the bioavailability of the 226 amino acid B domain FVIII variant alone was similar to that obtained with co-formulation with VWF. Hence, for this variant with a longer B-domain, VWF did not increase the bioavailability.

Example 10

Construction of Expression Vectors Encoding FVIII Molecules

Plasmid with insert encoding the F8-500 FVIII molecule (F8-500 equals turoctocog alfa/N8 encoding sequence) was used for production of FVIII. Starting at the N-terminus, the F8-500 vector encodes the FVIII heavy chain without the B domain (amino acids 1-740), a 21 amino acid linker (SFSQN-SRHSQNPVVKRHR—SEQ ID NO 2), and the FVIII

light chain (amino acids 1649-2332 of full-length wild-type human FVIII). The sequence of the 21 amino acid linker is derived from the FVIII B domain and consists of amino acids 741-750 and 1638-1648 of full length wild-type human FVIII. Fragments of FVIII cDNA were amplified from full length FVIII cDNA and inserted into F8-500 coding plasmid giving rise to DNA constructs encoding the BDD FVIII.

Constructs encoding F8-500D-HIS-C2-linked-(GGGS)₆-hFc(IgG1), F8-500D-HIS-C2-linked-(GGGS)₆-mFc(IgG2A), and F8-500D-HIS-C2-linked-(GGGS)₆-albumin were established as described in the following. The internal BamHI site (aa 604-606) in F8-500 coding DNA was eliminated by site-directed mutagenesis and DNA encoding the flexible (GGGS)₆ linker was inserted 3' to the coding region. A new BamHI site was introduced in the 3' end of the linker-coding DNA in order to ease cloning of C-terminal fusion partners between BamHI and NotI sites. Thus, a construct encoding F8-500-C2-linked-(GGGS)₆ was generated. DNA encoding human Fc (IgG1), mouse Fc (IgG2a), and human serum albumin was amplified.

The PCR products were inserted between the BamHI and Not I sites of the F8-500-C2-linked-(GGGS)₆ coding vector giving rise to constructs encoding F8-500-C2-linked-(GGGS)₆-hFc(IgG1), F8-500-C2-linked-(GGGS)₆-mFc(IgG2A), and F8-500-C2-linked-(GGGS)₆-albumin. A SphI/ClaI restriction fragment from the latter constructs were transferred to a F8-500D-His coding constructs in order to generate F8-500D-HIS-C2-linked-(GGGS)₆-hFc(IgG1)-, F8-500D-HIS-C2-linked-(GGGS)₆-mFc(IgG2A)-, and F8-500D-HIS-C2-linked-(GGGS)₆-albumin coding constructs.

For transient expression as described in Example 11, DNA constructs consisting of the mammalian expression vector pTT5 with insert encoding BDD FVIII were utilized. For generation of stable cell lines producing BDD FVIII, the vector pTSV7 is utilized. This vector encodes dihydrofolate reductase allowing selection of transfected cells with the dihydrofolate reductase system. A SpeI/AgeI restriction fragment from a pTT5-derived vector encoding F8-500D-His was transferred to a pTSV7-derived vector encoding F8-500 leading to construct #1917 consisting of pTSV7 with insert encoding F8-500D-His.

Example 11

Transient Expression of FVIII

HKB11 cells at a density of 0.9-1.1 \times 10⁶ were transfected with a complex of plasmid (0.7 mg/l or 1.0 mg/l) and the transfection agent, 293Fectin (Invitrogen) (1.0 ml/l or 1.4 ml/l). The transfection complex was prepared by diluting the plasmid and the transfection separately, mixing the two solutions, and incubating the mixture at room temperature for 20 minutes. The complex mixture was added to the cell suspension and the suspension was incubated in shaker incubator for 4 or 5 days at 36.5° C. or 37° C. and at 5% or 8% CO₂. Cell culture harvests were analysed by chromogenic FVIII assay as described in Example 14 and/or filtered through a 0.22 μ m membrane filter and utilized for purification of FVIII as described in Example 13.

Example 12

Stable Cell Line Expressing FVIII

Serum-free adapted CHO-DUKX-B11 cells were transfected with the expression plasmid construct #1917 described in Example 10 and encoding the FVIII F8-500D-His. Transfected cells were selected with the dihydrofolate reductase system and cloned by limiting dilution. Clones were screened for FVIII production by ELISA and chromogenic activity assay. The clone GedT019A was selected for upscaling. The

cells were transferred to a bioreactor. The F8-500D-His protein was purified from cell culture harvests as described in Example 13

Example 13

Purification of FVIII

A column was packed with the resin VIIISelect (GE Healthcare), with the dimensions 1.6 cm in diameter and 4 cm in bed height giving 8 mL, and was equilibrated with 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80+250 mM NaCl, pH7.3 at 500 cm/h. The culture filtrate prepared as described in Example 3 was applied to the column, and the column was subsequently washed with first equilibration buffer and then 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80+1.5M NaCl, pH7.3. The bound FVIII was eluted isocratically at 90 cm/h with 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80+1M Ammoniumacetate+6.5M Propylenglycol, pH7.3. The fractions containing FVIII were pooled and diluted 1:10 with 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80, pH7.3 and applied to a column packed with F25-Sepharose (Thim et al., Haemophilia, 2009). The column dimension was 1.6 cm in diameter and 2 cm in bed height giving 4 mL in column volume. The column was equilibrated at 180 cm/h with 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80+150 mM NaCl+1M Glycerol, pH7.3 prior to application. After application the column was washed first with equilibration buffer and then 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80+650 mM NaCl, pH7.3. The bound FVIII was isocratically eluted with 20 mM Imidazole+10 mM CaCl₂ 0.01% Tween80+2.5M NaCl+50% (v/v) Ethylenglycol, pH7.3 at 30 cm/h. The fractions containing FVIII were pooled and diluted 1:15 with 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80, pH7.3, except FVIII-variants with deletions of the a3 domain which were diluted 1:45 in the same buffer. The diluted pool was applied to a column packed with Poros 50HQ (PerSeptive Biosystem), with the column dimensions 0.5 cm in diameter and 5 cm in bed height giving 1 mL in column volume. The column was equilibrated at 300 cm/h with 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80+50 mM NaCl+1M Glycerol, pH7.3 prior to application. The column was washed with equilibration buffer before the elution using a linear gradient over 5 column volumes from equilibration buffer to 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80+1M NaCl+1M Glycerol, pH7.3. The fractions containing FVIII were pooled and the pool was stored at -80° until use.

The FVIII molecules with HIS-tag were purified essentially as described above, however the second purification step (F25-sepharose) was exchanged to Chelating Sepharose FF (GE Healthcare) charged with 2 column volumes of 1M NiSO₄. The column dimension was 0.5 cm in diameter and 5 cm bed height giving 1 mL column volume. The column was equilibrated with 30 mM Imidazole+10 mM CaCl₂+0.01% Tween80+1.5M NaCl, pH7.3 at 180 cm/h prior to application. After application the column was washed with 30 column volumes of equilibration buffer prior to elution using a linear gradient over 5 column volumes to 250 mM Imidazole+10 mM CaCl₂+0.01% Tween80+1.5M NaCl, pH7.3. The fractions containing FVIII were pooled and diluted 1:30 with 20 mM Imidazole+10 mM CaCl₂+0.01% Tween80, pH7.3. The final purification step (Poros 50HQ) was performed as described above.

Example 14

FVIII Activity in Cell Culture Harvests Measured by Chromogenic Assay

The FVIII activity (FVIII:C) of the rFVIII compound was evaluated in a chromogenic FVIII assay using Coatest SP reagents (Chromogenix) as follows: rFVIII samples and a

FVIII standard (Coagulation reference, Technoclone) were diluted in Coatest assay buffer (50 mM Tris, 150 mM NaCl, 1% BSA, pH 7.3, with preservative). Fifty µl of samples, standards, and buffer negative control were added to 96-well microtiter plates (Spectraplates MB, Perkin Elmer). All samples were tested diluted 1:100, 1:400, 1:1600, and 1:6400. The factor IXa/factor X reagent, the phospholipid reagent and CaCl₂ from the Coatest SP kit were mixed 5:1:3 (vol:vol:vol) and 75 µl of this added to the wells. After 15 min incubation at room temperature, 50 µl of the factor Xa substrate 5-2765/thrombin inhibitor I-2581 mix was added and the reactions were incubated 5 min at room temperature before 25 µl 1 M citric acid, pH 3, was added. The absorbance at 405 nm was measured on an Envision microtiter plate reader (Perkin Elmer) with absorbance at 620 nm used as reference wavelength. The value for the negative control was subtracted from all samples and a calibration curve prepared by linear regression of the absorbance values plotted vs. FVIII concentration. The yields of the present FVIII relative to that of the F8-500 protein are shown in Table 1.

Example 15

FVIII Activity in Purified Samples Measured by Chromogenic Assay

The FVIII activity (FVIII:C) of the rFVIII compound was evaluated in a chromogenic FVIII assay using Coatest SP reagents (Chromogenix) as follows: rFVIII samples and a FVIII standard (e.g. purified wild-type rFVIII calibrated against the 7th international FVIII standard from NIBSC) were diluted in Coatest assay buffer (50 mM Tris, 150 mM NaCl, 1% BSA, pH 7.3, with preservative). Fifty µl of samples, standards, and buffer negative control were added to 96-well microtiter plates (Nunc) in duplicates. The factor IXa/factor X reagent, the phospholipid reagent and CaCl₂ from the Coatest SP kit were mixed 5:1:3 (vol:vol:vol) and 75 µl of this added to the wells. After 15 min incubation at room temperature 50 µl of the factor Xa substrate S-2765/thrombin inhibitor I-2581 mix was added and the reactions incubated 10 min at room temperature before 25 µl 1 M citric acid, pH 3, was added. The absorbance at 415 nm was measured on a Spectramax microtiter plate reader (Molecular Devices) with absorbance at 620 nm used as reference wavelength. The value for the negative control was subtracted from all samples and a calibration curve prepared by linear regression of the absorbance values plotted vs. FVIII concentration. The specific activity was calculated by dividing the activity of the samples with the protein concentration determined by HPLC. For HPLC, the concentration of the sample was determined by integrating the area under the peak in the chromatogram corresponding to the light chain and compare with the area of the same peak in a parallel analysis of a wild-type rFVIII, where the concentration was determined by amino acid analyses. The results are shown in Table 1.

Example 16

FVIII Activity in Purified Samples Measured by One-Stage Clot Assay

FVIII activity (FVIII:C) of the rFVIII compounds was further evaluated in a one-stage FVIII clot assay as follows: rFVIII samples and a FVIII standard (e.g. purified wild-type rFVIII calibrated against the 7th international FVIII standard from NIBSC) were diluted in HBS/BSA buffer (20 mM hepes, 150 mM NaCl, pH 7.4 with 1% BSA) to approximately 10 IU/ml followed by 10-fold dilution in FVIII-deficient plasma containing VWF (Dade Behring or Siemens). The samples were subsequently diluted in HBS/BSA buffer. The

APTT clot time was measured on an ACL300R or an ACL9000 instrument (Instrumentation Laboratory) using the single factor program. FVIII-deficient plasma with VWF (Dade Behring or Siemens) was used as assay plasma and SynthASil, (HemosIL™, Instrumentation Laboratory) as aPTT reagent. In the clot instrument, the diluted sample or

standard is mixed with FVIII-deficient plasma, aPTT reagents at 37° C. Calcium chloride is added and time until clot formation is determined by turbidity. The FVIII activity in the sample is calculated based on a standard curve of the clot formation times of the dilutions of the FVIII standard. The results are shown in table 1.

TABLE 1

Yields and specific activities of different BDD FVIII molecules ("His-tagged" for easier purification).				
Compound	B domain amino acids	Yield by transient transfection (relative to F8-500)	Specific activity measured by chromogenic assay (IU/mg)	Specific activity measured by one-stage clot assay (IU/mg)
F8-500E-His	741-857 + 1637-1648	0.7	10501	9122
F8-500L-His	741-914 + 1637-1648	0.6	10330	8282
F8-500M-His	741-954 + 1637-1648	0.6	12404	10259
F8-500D-His	741-965 + 1637-1648	0.3	9015	9579
F8-500G-His	741-965 + 1637-1648	0.7	11507	9822
Amino acid replacements:				
N757Q-N784Q-N828Q-N900Q-N943Q-N963Q				
F8-500N-His	741-1003 + 1637-1648	0.4	—	—
F8-500H-His	741-1020 + 1637-1648	0.7	10027	10541
F8-500I-His	741-1079 + 1637-1648	0.7	—	—
F8-500J-His	741-1206 + 1637-1648	0.6	—	—
F8-500F-His	741-1261 + 1637-1648	0.3	5691	4855
F8-500K-His	741-1309 + 1637-1648	0.4	—	—
F8-500-His2-4N	741-914 + 1637-1648	0.6	—	—
F8-500-His2-5N	741-954 + 1637-1648	0.7	—	—
F8-500-His2-6N	741-968 + 1637-1648	0.6	14088	12784
F8-500-His2-7N	741-1003 + 1637-1648	0.5	7211	7542
F8-500-His2-8N	741-1018 + 1637-1648	0.7	8664	7481
F8-500-His2-10N	741-1070 + 1637-1648	0.6	12391	8253
F8-500-His2-11N	741-1230 + 1637-1648	0.5	—	—
F8-500-His2-15N	741-1301 + 1637-1648	0.4	—	—
F8-500D-His-D519V-E1984A	741-965 + 1637-1648	0.5	15282	9729
F8-500D-His-C2 linked-(GGGS)6-hFc(IgG1)	741-965 + 1637-1648	0.6	—	—
F8-500D-His-C2 linked-(GGGS)6-mFc(IgG2a)	741-965 + 1637-1648	0.6	13509	8858
F8-500D-His-C2 linked-(GGGS)6-albumin	741-965 + 1637-1648	0.7	12226	5852

Example 17

Construction of Expression Vectors Encoding VWF Fragments

DNA fragments encoding the VWF signal peptide, followed by different C-terminally truncated versions, the VWF D' domain and the VWF D3 domain, an Ala-Leu-Ala spacer and a HPC4 tag were generated by polymerase chain reaction (PCR) using plasmid pLC095 as template (Plasmid pLC095 is described in Example 26. The primer JP1000 was used as forward primer in all PCR reactions in combination with the reverse primers JP1001-JP1008 shown in Table 2.

TABLE 2

Forward primer	Forward primer Sequence (5'-3')
JP1000 VWF-HindIII S	CTAAGCGTAAGCTTGGCCACCATGATTCTCTGCCAGATTGCGG (SEQ ID NO 23)

TABLE 2-continued

Reverse primer	Reverse primer Sequence (5'-3')
JP1001 VWF 764-828	TGGTCCTCAGCTAGCGCGGACACCTTTCCAGGGCCACA C (SEQ ID NO 24)
JP1002 VWF 764-865	TGGTCCTCAGCTAGCGCGCATCACACATGGTCTGTG C (SEQ ID NO 25)
JP1003 VWF 764-1035	TGGTCCTCAGCTAGCGCTCTGGTGTGAGCAGTGCAG CTC (SEQ ID NO 26)
JP1004 VWF 764-1041	TGGTCCTCAGCTAGCGCTGAGTCCAGAGGCACTTTTCTGG (SEQ ID NO 27)
JP1005 VWF 764-1045	TGGTCCTCAGCTAGCGGTGGCAGGGGATGAGTCCAGA G (SEQ ID NO 28)
JP1006 VWF 764-1250	TGGTCCTCAGCTAGCGCGCATCTGTGGGAGGCACCACC (SEQ ID NO 29)
JP1007 VWF 764-1261	TGGTCCTCAGCTAGCGCTCTCCACATACAGAGTGGTG (SEQ ID NO 30)
JP1008 VWF 764-1268	TGGTCCTCAGCTAGCGCATCGTGCAACGGCGTTCCGAG (SEQ ID NO 31)

The PCR products were digested with HindIII and NheI and were subsequently cloned into a HindIII and NheI digested pJSV164 vector using Rapid DNA Ligation kit (Roche Diagnostics GmbH, Mannheim, Germany). pJSV164 is a pTT5 based expression vector (Yves Durocher, CNRC, Montreal, Canada) containing a CD33 signal peptide and a HPC4 tag. Digestion of pJSV164 with HindIII and NheI removes the CD33 signal peptide and allows cloning of the gene of interest in frame with the HPC4 tag to generate an expression cassette encoding a C-terminally HPC4 tagged gene of interest in which the gene of interest and the HPC4 tag is separated by an Ala-Leu-Ala linker peptide. The ligation reactions were transformed into Top10 cells (Life Technologies, Carlsbad, Calif., USA).

The resulting eight plasmids were named as shown in Table 3. The amino acid sequences of the generated proteins are outlined in SEQ ID NO 4, 5, 6, 7, 8, 11 and 16.

TABLE 3

Vector name	Insert
pJSV343	VWF 764-828-HPC4 (SEQ ID NO 4)
pJSV344	VWF 764-865-HPC4 (SEQ ID NO 5)

TABLE 3-continued

Vector name	Insert
pJSV345	VWF 764-1035-HPC4 (SEQ ID NO 6)
pJSV346	VWF 764-1041-HPC4 (SEQ ID NO 7)
pJSV347	VWF 764-1045-HPC4 (SEQ ID NO 8)
pJSV348	VWF 764-1250-C1099/1142S-HPC4 (SEQ ID NO 11)
pJSV349	VWF 764-1261-C1099/1142S-HPC4 (SEQ ID NO 14)
pJSV350	VWF 764-1268-C1099/1142S-HPC4 (SEQ ID NO 15)

Example 18

Construction of Expression Vectors Encoding VWF Fragments (2)

Three additional HPC4 tagged, truncated variants of VWF were generated by Ligation independent cloning (LIC) using pJSV348 (see Example 17) as template. Three independent PCR reactions were set-up on pJSV438 using the primers shown in Table 4.

TABLE 4

Fragment	Primer name	Primer sequence (5'-3')
VWF (864-1250)-HPC4 (SEQ ID NO 12)	VWF (864-1250)-HPC4 S	GGGACCCCTTGTGATGCCACGTGCTCCACGATCG G (SEQ ID NO 32)
	VWF (864-1250)-HPC4 AS	GCACGTGGCATCACAAAGGGTCCCTGGCAAATG AG (SEQ ID NO 33)
VWF (764-1128)-HPC4 (SEQ ID NO 9)	VWF (764-1128)-HPC4 S	TTGTGCCCCAGGAGGACCAAGTAGATCCGCGGC TC (SEQ ID NO 34)
	VWF (764-1129)-HPC4 AS	TACTTGGTCCTCTGGGGGCACAATGTGGCCGTC (SEQ ID NO 35)

TABLE 4-continued

Fragment	Primer name	Primer sequence (5'-3')
VWF (764-1198)-HPC4 (SEQ ID NO 10)	VWF (764-1198) - HPC4 S	GACTGTCCAGTGGAGGACCAAGTAGATCCGCGG (SEQ ID NO 36)
	VWF (764-1198) - HPC4 AS	TTGGTCCTCCACTGGACAGTCTTCAGGGTCAA (SEQ ID NO 37)

The three PCR fragments VWF(864-1250)-HPC4, VWF (764-1128)-HPC4 and VWF(764-1198)-HPC4 were 5685/5610/5817 by in size respectively. The PCR fragments were DpnI treated to remove methylated template DNA. The PCR fragments were subsequently purified from gel and were self-ligated by LIC using the In-Fusion HD Cloning Kit (Clontech, Mountain View, Calif., USA) to generate circular DNA fragments and subsequently transformed into Top10 cells (Life Technologies, Carlsbad, Calif., USA).

The resulting three plasmids were named as shown in Table 5. The amino acid sequences of the generated proteins are outlined in SEQ ID NOs 12, 9, and 10.

TABLE 5

Vector name	Insert
pJSV405	VWF(864-1250)-C1099/1142S-HPC4 monomer (SEQ ID NO 12)
pJSV406	VWF(764-1128)-C1099S-HPC4 monomer (SEQ ID NO 9)
pJSV407	VWF(764-1198)-C1099/1142S-HPC4 monomer (SEQ ID NO 10)

Example 19

Transient Expression of VWF Fragments
Human embryonic kidney 293 6E suspension cells at a density of 0.9-1.1x10⁶ cells/ml were transfected with a complex of VWF fragment coding plasmid (0.7 mg/l or 1.0 mg/l) and the transfection agent 293Fectin (Invitrogen) (1.0 ml/l or 1.4 ml/l). The transfection complex was prepared by diluting the plasmid and the transfection separately, mixing the two solutions, and incubating the mixture at room temperature for 20 minutes. The complex mixture was added to the cell suspension and the suspension was incubated in shaker incubator for 5 days at 36.5° C. or 37° C. and at 5% or 8% CO₂. Cell culture harvests were filtered through a 0.22 µm membrane filter and utilized for purification of VWF fragment as described in Example 22.

Example 20

Preparation of Dimer Forms of VWF Fragments
In the native full length VWF molecule (SEQ ID NO 22) two cysteine residues in the N-terminal part of the molecule are supposed to participate in the dimerization and/or multimerization of VWF: Cys1099 and Cys1142.
In all of the monomeric fragments of the sequences (SEQ ID NO 10, SEQ ID NO 11, SEQ ID NO 12, SEQ ID NO 13, SEQ ID NO 14, SEQ ID NO 15, SEQ ID NO 16, SEQ ID NO 17, SEQ ID NO 18, SEQ ID NO 19, SEQ ID NO 20, and SEQ ID NO 21) two cysteine residues (Cys1099 and Cys1142) are mutated to other amino acid residues so that the expressed molecule is not able to form dimers/multimers. A monomeric fragment of SEQ ID NO 9 is generated by mutating Cys 1099 to another amino acid residue.

In some cases, a dimeric form of the VWF fragments is wanted. This can be accomplished in several ways:

One method to accomplish dimer formation is to keep the two residues at position 1099 and position 1142 as cysteines. In order to make a recombinant dimeric molecule, the cDNA encoding the desired VWF fragment is including the presequence of VWF e.g the D1D2 sequence of VWF (amino acid residues 23-763 of SEQ ID NO 22). This will, during processing in the golgi apparatus align two monomers of a given VWF fragment in a configuration allowing a dimeric molecule to be formed with two disulphide bonds in which Cys1099 in monomer 1 is connected to a Cys1099 in monomer 2 and Cys1142 in monomer 1 is connected to Cys1142 in monomer 2.

Another method to accomplish dimer formation is to avoid the inclusion of the presequence (amino acid residues 23-763 of SEQ ID NO 22) and simply let a recombinant VWF fragment with Cys in position 1099 and 1142 form a dimeric molecule. This can in principle result in a series of different dimers e.g.:

- Cys1099-Cys1099/Cys1142-Cys1142 (two disulphide bonds—like above)
- Cys1099-Cys1142/Cys1099-Cys1142 (two disulphide bonds)
- Cys1099-Cys1099 (one disulphide bond)
- Cys1142-Cys1142 (one disulphide bond)
- Cys1099-Cys1142 (one disulphide bond)

Yet another method to accomplish dimer formation may be to replace one of the cysteine residues 1099 or 1142 with other amino acid residues (e.g. Serine, Arginine).

If Cys1099 is replaced with a non-Cysteine residue, the molecule may form a dimer by establishment of a disulphide bond between Cys1142 in monomer 1 with Cys1142 in monomer 2.

If Cys1142 is replaced with a non-Cysteine residue, the molecule may form a dimer by establishment of a disulphide bond between Cys1099 in monomer 1 with Cys1099 in monomer 2.

The dimeric forms mentioned above may be constructed either with or without the D1D2 presequence of VWF (amino acid residues 23-763 of SEQ ID NO 22).

The different monomeric and dimeric forms will have different properties with regards to their binding to FVIII, their ease of production and their effect on bioavailability of FVIII when injected subcutaneously as a co-formulation.

Example 21

Evaluation of Binding of VWF and VWF Fragments to FVIII Using a Competition ELISA

In order to investigate the binding of the different VWF fragments to FVIII the following method is used. Briefly, human VWF is coated in a microtiterplate and incubated overnight at 4° C. After blocking, a solution with pre-incubated FVIII (1 nM) and VWF/VWF-fragment is added to the

plate, followed by detection with biotinylated anti FVIII antibody and streptavidin-peroxidase S-POD (1:20000). The absorbance is measured at 450/620 nm. The IC50 values are shown in Table 6.

TABLE 6

Compound number	Domain/comment	VWF fragment sequence	Derived from SEQ ID NO	
			IC50 (Ki)	
2304	TIL/E'	VWF(764-865)-ALA-HPC4 monomer	5	2.0 μ M
2306	TIL/E'/VWD3 II	VWF(764-1041)-ALA-HPC4 monomer	7	2.2 μ M
2307	TIL/E'/VWD3 III	VWF(764-1045)-ALA-HPC4 monomer	8	2.0 μ M
2308	TIL/E'/D3 I	VWF(764-1250)-C1099/1142S-ALA-HPC4 monomer	11	12 nM
2309	TIL/E'/D3 II	VWF(764-1261)-C1099/1142S-ALA-HPC4 monomer	14	10 nM
2310	TIL/E'/D3 III	VWF(764-1268)-C1099/1142S-ALA-HPC4 monomer	16	15 nM
0170	TIL/E'/D3/A1 III	VWF(764-1464)-C1099/1142S-HPC4 monomer	19	12 nM
0194	TIL/E'/D3/A1 III	VWF(764-1464)-C1099S-HPC4 monomer	19	8.0 nM
0240	TIL/E'/D3/A1 III dimer	VWF(764-1464)-HPC4 dimer	19	0.7 nM
0001	D3 I	VWF(864-1250)-C1099/1142S-ALA-HPC4 monomer	12	20 μ M
0003	TIL/E'/VWD3/C8-3/TIL-3	VWF(764-1198)-C1099/1142S-ALA-HPC4 monomer	10	28 nM
0314	Plasma derived full length VWF	VWF (764-2813)	22	1.1 nM

These differences in FVIII binding between different fragments could indicate different effects in a subcutaneously administered FVIII co-formulation. The IC50 values are also being used to determine the optimal VWF and FVIII concentrations in the co-formulation mixtures.

Example 22

Purification and Characterisation of HPC4-Tagged VWF Fragments

Some VWF fragments are cloned and expressed with a C-terminal HPC4 tag: EDQVDPRLIDGK (SEQ ID NO 38). Sometimes an additional linker with the sequence of ALA is introduced between the VWF fragment and the HPC4 tag. After cloning, expression and cell culturing the cell media is added CaCl₂ to a final concentration of 1 mM. The media is passed over an anti-HPC4 column. The column is equilibrated with 20 mM HEPES, 100 mM NaCl, 1 mM CaCl₂, pH=7.5. After application of the cell media, the column is washed with 20 mM HEPES, 1M NaCl, 1 mM CaCl₂, pH=7.5 and the HPC4-tagged VWF fragment is subsequently eluted with 20 mM HEPES, 100 mM NaCl, 5 mM EDTA, pH=7.5. The pool from the anti-HPC4 column is added 3 volumes of water to reduce the conductivity and applied onto a Mono Q column. Prior to the application the Mono Q column is equilibrated with 20 mM HEPES, 100 mM NaCl, 5 mM EDTA, pH=7.5. The Mono Q column is washed with 20 mM HEPES, 100 mM NaCl, pH=7.5 and the VWF fragment is eluted with a gradient from 100 mM NaCl to 2M NaCl in 20 mM HEPES, 10 mM CaCl₂, pH=7.5.

The purified protein is characterised by 1) SDS-gel electrophoreses, 2) analytical HPLC and 3) amino acid sequence analysis.

Purification and Characterisation of Non-Tagged VWF Fragments.

After cloning, expression and cell culturing the cell media is passed over an anti-VWF column. The anti-VWF antibody recognise amino acid residue number 764-865 of VWF (SEQ ID NO 5). The column is equilibrated with 20 mM HEPES, 100 mM NaCl, pH=7.5. After application of the cell media, the column is washed with 20 mM HEPES, 1M NaCl, pH=7.5 and the VWF fragment is subsequently eluted with 50 mM

acetic acid, 100 mM NaCl, pH=4.0. The pool from the anti-VWF column is adjusted to pH=7.5 and applied onto a Mono Q column. Prior to the application the Mono Q column is equilibrated with 20 mM HEPES, 100 mM NaCl, pH=7.5.

The Mono Q column is washed with 20 mM HEPES, 100 mM NaCl, pH=7.5 and the VWF fragment is eluted with a gradient from 100 mM NaCl to 2M NaCl in 20 mM HEPES, pH=7.5.

The purified VWF fragment is characterised by 1) SDS-gel electrophoreses, 2) analytical HPLC and 3) amino acid sequence analysis.

Example 23

Evaluation of VWF Fragments Binding to FVIII by Using Isothermal Titration Calorimetry

All protein samples are dialyzed in 50 mM Hepes pH 7.4, 150 mM NaCl, 10 mM CaCl₂ buffer. Each iTC experiment involves filling the iTC cell with FVIII (approximately 250 μ L) and the syringe with VWF variants (approximately 40 μ L). Temperature is set as required and the protein sample is allowed to equilibrate under given experimental conditions (approximately 10 minutes). Typically 17-20 injections (of 2-2.5 μ L) of VWF variants into cell, containing FVIII, are performed. The first injection is always of 0.2 μ L and is discarded from the final data analysis in order to account for diffusion during equilibration step. Stirring speed is set between 700-1000 rpm. Filter period for data collection is 5 sec with a high feedback mode setting. Each titration is spaced by 120 sec. Appropriate control experiments are performed. Raw data is processed to set baseline and integrated to obtain a final isotherm. This binding isotherm is fit to a single-site model to yield K_d, stoichiometry (n), Δ H, and Δ S values to complete characterization of VWF variant binding to FVIII. An example binding isotherm is shown in FIG. 9. These data are being used for determining the optimal concentrations of the FVIII and the VWF fragment in co-formulations intended for subcutaneous administrations.

Example 24

Subcutaneous Administration in FVIII Knockout Mice

Test compounds were prepared as follows: Test compounds were formulated in 18 mg/ml NaCl, 3 mg/ml saccharose, 1.5 mg/ml L-histidine, 0.1 mg/ml polysorbate 80, 0.25 mg/ml CaCl₂, pH ~7.3. For test formulations containing VWF or VWF fragments the % FVIII bound by VWF in the

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co-formulation was calculated using the available IC50 (Ki) values as described above in example 21 (table 6) assuming $K_i=K_d$ or the K_d values obtained as described in example 23.

FVIII KO mice, exon 16 knock-out in a mixed background of C57Bl/6 and SV129, bred at Taconic M&B (B6.129S4-F8tm1Kaz/J) with an approximate weight of 22 g were dosed subcutaneously in the flank with FVIII in combination with various proteins, 6-9 mice with each test compound. The dose volume was 5 ml/kg or 0.25 ml/kg if indicated in table 7.

Blood was sampled at 9 time points from 0-96 h, n=2-3 mice/time point, 3 blood samples from each mice in a sparse sampling regime. The mice were anaesthetized by Isoflurane/O₂/N₂O prior to blood sampling via the retroorbital plexus. 45 µl of blood was stabilised with 5 µl of sodium-citrate (0.13 M) and added 200 µl FVIII Coatest SP buffer (50 mM TRIS-HCl, 1% BSA, Ciprofloxacin 10 mg/L, pH 7.3). After cen-

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trifugation at 4000 g for 5 minutes at room temperature, the supernatants were immediately frozen on dry ice before storage at -80° C. prior to analysis.

Samples were analysed with regards to FVIII chromogenic activity as described by Ovlisen K et al. J. Thromb. Haemost, 2008, 6: 969-975 and by FVIII antigen analysis using two FVIII light chain antibodies (4F45 and 4F11) in a FVIII LOCI assay (Luminescence oxygen channelling immunoassay).

Mean plasma concentration versus time data were analysed by non-compartmental analysis using WinNonlin Phoenix (Pharsight Corporaton) estimating the given pharmacokinetic parameters. The bioavailability was estimated using a previous i.v. pharmacokinetic study of N8 or N8-GP in the FVIII KO mouse strain.

The s.c. FVIII bioavailabilities of the test compounds are shown in table 7 below and in FIGS. 7 and 8.

TABLE 7

FVIII Bioavailability values of a series of different FVIII molecules and FVIII/VWF fragment co-formulations obtained with s.c. administration in FVIII k/o mice.					
FVIII	FVIII Dose	Co-Formulation Protein	Molar Ratio	FVIII Saturation	F %
Turoctocog alfa	5000	(764-1464) monomer VWF	1	87%	7.3
rFVIII derived from the full-length sequence (Kogenate ®)	2500	(764-1464) Dimer VWF	1	82%	7.4
Turoctocog alfa	2500	(764-1250) Monomer VWF	1	82%	7.6
Turoctocog alfa	2500	(764-1041) Monomer VWF	34	82%	7.8
Turoctocog alfa	2500	(764-828) Monomer VWF	1	12%	1.4
Turoctocog alfa	2500	(764-865) Monomer VWF	1	12%	2.7
Turoctocog alfa	2500	(764-1045) Monomer VWF	1	12%	2.0
Turoctocog alfa	2500	(764-865) Monomer VWF	34	83.3%	4.3
Turoctocog alfa	2500/0.25 ml/kg	(764-1041) Monomer VWF	3x	85.5%	5.03
Turoctocog alfa	2500/0.25 ml/kg	(764-865) Monomer VWF	3x	86.5%	1.9
Turoctocog alfa	2500/0.25 ml/kg	(764-1464) Dimer VWF	1x	99%	8.4
Turoctocog alfa	2500	(764-1464) Murine monomer VWF	1	82%	5.6
Turoctocog alfa	2500	Human serum Albumin	611	Not applicable	3.7
Turoctocog alfa	2500	plasma derived full length VWF	1	99%	0.0
Turoctocog alfa	5000	(764-1464) monomer VWF	7.7	99%	8.2
Turoctocog alfa	5000	(764-1464) monomer VWF	3	99%	6.7
Turoctocog alfa	5000	(764-1464) monomer VWF	1	87%	7.3
Turoctocog alfa	5000	None	Not applicable	Not applicable	2.3
FVIII with a 226 aa B domain	5000	None	Not applicable	Not applicable	4.3
FVIII with a-226 aa B domain	5000	(764-1464) monomer VWF	7.7	0.99	7.0
N8-GP	2500	(764-1464) monomer VWF	1	0.82	27
N8-GP	10000	(764-1464) monomer VWF	7.7	0.99	47
N8-GP	2500	(764-1464) monomer VWF	7.7	0.99	36
N8-GP	2500	(764-1464) Dimer VWF	1	0.99	33
FVIII-K1804-Hep157	2500	(764-1464) monomer VWF	1	0.82	50

TABLE 7-continued

FVIII Bioavailability values of a series of different FVIII molecules and FVIII/VWF fragment co-formulations obtained with s.c. administration in FVIII k/o mice.					
FVIII	FVIII Dose	Co-Formulation Protein	Molar Ratio	FVIII Saturation	F %
FVIII-K1804-Hep157	2500	None	Not applicable	Not applicable	27
PSA40Kd-O-Glycan-N8	2500	(764-1464) monomer VWF	1	0.82	8.8
PSA40Kd-O-Glycan-N8	2500	None	Not applicable	Not applicable	6.1
40kDa-PEG-FVIII-K2092A + F2093A	10000	None	Not applicable	Not applicable	20
N8-GP	10000	4F30 FVIII reduced uptake antibody	5	0.99	11
N8-GP	1000	Hirudin	0.5 mg/kg	Not applicable	7.6
N8-GP	10000	Hyaluronidase	0.5 activity ratio	Not applicable	8.4
N8-GP	20000	None	Not applicable	Not applicable	28
N8-GP	10000	None	Not applicable	Not applicable	19
N8-GP	2500	None	Not applicable	Not applicable	14
N8-GP	1000	None	Not applicable	Not applicable	17

The left column "FVIII" denotes the FVIII compound used in the experiment.

The column labelled "FVIII dose" denotes the FVIII dose (IU/kg) used in the experiment,

the column labelled "co-formulation protein" denotes the co-formulated protein (if any) used in the experiment.

The column labelled "Molar ratio" denotes the molar ratio to FVIII of the protein in the co-formulation.

The column labelled "FVIII Saturation" denotes the calculated fraction of FVIII that is binding the co-formulated protein at the concentrations used in the experiment.

The column labelled "F %" denotes the bioavailability of FVIII obtained in the experiment.

The s.c. bioavailability of FVIII co-formulated with a VWF fragment appear to depend on the saturation of the FVIII VWF binding sites in the co-formulation rather than on the VWF fragment length. The shortest VWF fragment, wherein a >80% saturation of FVIII was achieved, was 764-865—this formulation displayed a FVIII bioavailability of 4.3% (34 molar excess of N8/turoctocog alfa over VWF fragment). The longest VWF fragment tested, under similar conditions with respect to saturation, was the 764-1464 fragment which resulted in a FVIII bioavailability of 7.3%. The dimer form of the 764-1464 dosed in a lower volume of 0.25 ml/kg resulted in a FVIII bioavailability of 8.4%.

Fragments shorter than 764-1250, which do not contain the entire D3 region, bind FVIII with a higher IC₅₀ (K_i) than longer fragments. Thus, 1 to 1 molar formulation of FVIII and VWF fragments shorter than 764-1250 displayed lower FVIII bioavailabilities, i.e. less than 4%.

The s.c. FVIII bioavailability-improving effect of VWF fragments according to the invention may thus be obtained by saturation of the FVIII VWF binding sites with VWF-fragment. Short VWF fragments with relatively low FVIII binding affinity should thus be used in higher ratios compared to longer VWF fragments with better binding FVIII binding properties in order to obtain a high degree of bioavailability.

FVIII derived from the full-length sequence (Kogenate®) displayed the same degree of bioavailability as FVIII with a truncated B domain (turoctocog alfa/N8) when co-formulated with the 764-1464 VWF fragment. This indicates that high FVIII bioavailability is not dependent on co-formulation with turoctocog alfa/N8 but is dependent on presence of the VWF fragment.

Co-formulation of FVIII (turoctocog alfa/N8) with full-length plasma-derived human VWF resulted in FVIII bio-

availability of about 0% thus demonstrating that only fragments of VWF are able to enhance bioavailability of FVIII. The reason for the lack of effect of the full-length VWF may be due to the presence of collagen binding site in the A3 domain which may result in binding and entrapment of. Preferred VWF fragments according to the present do thus not comprise the A3 domain. Alternatively or additionally, the multimerisation capabilities of full-length VWF produces large multimers that restricts systemic absorption due to size of the complex. The data indicates that also longer VWF fragments (preferably without the A3 domain) than those tested in table 7 will have the same beneficial effect on FVIII bioavailability.

Serum albumin did not improve the s.c. bioavailability of FVIII (turoctocog alfa/N8). Thus, presence of additional protein in a FVIII formulation does not appear to increase the s.c. bioavailability of FVIII—unless this protein is a VWF fragment according to the present invention.

VWF dose was not critical for FVIII s.c. bioavailability as seen for molar ratios between 1:1 and 1:7.7 of FVIII:VWF fragment. The critical factor for achieving a high FVIII bioavailability thus appear to be a high degree of FVIII saturation (binding) with VWF fragment. All compositions in these experiments comprising a calculated saturation of N8 of at least 86.8% thus resulted in similar bioavailabilities. VWF fragments according to the invention may thus protect FVIII at the s.c. injection site.

FVIII with a 226 amino acid (aa) B domain (SEQ ID NO 3), displayed a higher s.c. FVIII bioavailability than turoctocog alfa/N8. However, bioavailability of this FVIII with a 226 aa B-domain was comparable to turoctocog alfa/N8 in connection with s.c. co-administration with the VWF-fragment 764-1464 (TIL'/E'/D3/A1) monomer. It may thus be speculated

that the additional amino acids in the 226 aa B-domain (compared to turoctocog alfa/N8) may protect clearance sites of FVIII in connection with extravascular administration thereof, meaning that such FVIII molecules might be used for s.c. administration with or without VWF according to the present invention.

FVIIIK1804C-HEP157, displayed a bioavailability of 50% dosed in co-administration with the VWF-fragment 764-1464 (TIL/E/D3/A1) monomer and a bioavailability of 27% dosed alone. PSA40 Kd-O-Glycan-N8, displayed a bioavailability of 8.8% dosed in co-administration with the VWF-fragment 764-1464 (TIL/E/D3/A1) monomer and 6.11% dosed alone. It may thus be speculated that conjugation of FVIII molecules with Heparosan polymers and/or Polysialic acid polymers either protects FVIII against breakdown/uptake in the sub cutis or enhances s.c. absorption. Heparosan appear to be more effective than Sialic acid polymers in enhancing the s.c. bioavailability. Both FVIII variants displayed higher bioavailability's when dosed together with VWF fragment.

N8-GP and FVIIIK1804C-HEP157+764-1464 (TIL/E/D3/A1) monomer and dimer, resulted in the highest bioavailability obtained. Bioavailability of N8-GP may thus be increased by increasing the dose or the concentration in the co-formulation. Dose volume was 5 ml/kg in all dosing's, thus the N8-GP concentration in the dosing solution was 2 times higher in the 20000 IU/kg dosing than in the 10000 IU/kg dosing. This resulted in 28% and 19% bioavailability respectively.

The 764-1464 dimer VWF fragment does not contain any mutations. The 764-1464 dimer VWF fragment binds stronger to Turoctocog alfa and N8-GP (table 6) but result in a similar bioavailability of FVIII as the monomer version of the fragment. This indicates that substituting Cys1099 and/or Cys1142 in the VWF fragments according to the invention does not influence the bioavailability of FVIII. Also, the binding affinity of VWF fragments to N8-GP does not influence the effect on bioavailability of N8-GP as long as more than 80% of the FVIII molecules are in complex with VWF fragment in co-formulation. Additionally, since the dimer version of VWF fragment 764-1464 improves the bioavailability, the maximum molecular weight of a desired VWF fragment may be equal to or larger than 158.8 KDa.

Co-formulation of N8-GP with hyaluronidase did not increase the FVIII bioavailability, indicating that the Hyaluron network in the extracellular matrix in the subcutis is not

In this formulation, 2000 IU/ml N8-GP was co-formulated with 1 mg/ml of 4F30 which means that 99.6% of FVIII was bound to the mAb also after in vivo dilution assuming a K_d of 0.6 nM, an in vivo dilution of 20x, a molecular weight for FVIII (turoctocog alfa/N8) of 170000 g/mol, a specific activity of 10000 IU/mg for turoctocog alfa/N8, and a molecular weight for 4F30 of 150000 g/mol. Also, the PEGylated FVIII with K2092A+F2093A mutations displayed decreased uptake in cells but the mutations did not improve the bioavailability compared to N8-GP. Inhibition of cellular FVIII uptake does thus not appear to be the mechanism by which co-formulated VWF fragments result in increased s.c. bioavailability of FVIII.

Example 25

Subcutaneous Administration in New Zealand White Rabbits

Test compounds were formulated in 18 mg/ml NaCl, 3 mg/ml saccharose, 1.5 mg/ml L-histidine, 0.1 mg/ml polysorbate 80, 0.25 mg/ml CaCl_2 , pH ~7.3. For test formulations containing VWF or VWF fragments the % FVIII bound by VWF was calculated using the available IC50 values (table 6) assuming $\text{IC}_{50} = K_d = K_a$.

Female New Zealand white rabbits weighing approximately 2-3 kg were used for the study. The animals were allowed free access to feed and water. The rabbits were dosed subcutaneously over the thigh with FVIII in combination with various proteins, 4-5 rabbits with each test compound. The dose volume was 0.2 ml/kg or 1 ml/kg.

Blood was sampled at 11 time points from 0 to 96 h with n=4-5 rabbits/time point. At each sampling time point, 1 ml blood was sampled from an ear artery by use of a 21G needle and EDTA coated tubes. The tubes were centrifuged within 10 minutes after blood drawing at 4000 G for 5 minutes and plasma separated. The samples were immediately frozen on dry ice before storage at -80°C . prior to analysis. The samples were analysed by FVIII antigen analysis using two FVIII light chain antibodies (4F45 and 4F11) in a FVIII LOCI assay (Luminescence oxygen channeling immunoassay).

Mean plasma concentration versus time data were analysed by non-compartmental analysis using WinNonlin Phoenix (Pharsight Corporation) estimating the given pharmacokinetic parameters. The bioavailability was estimated using pharmacokinetics of FVIII (turoctocog alfa/N8) and N8-GP administered i.v. to rabbits.

The obtained bioavailabilities are shown in table 8.

TABLE 8

FVIII	FVIII Dose/dose volume	co formulation protein	Molar ratio co-formulation protein:FVIII	Saturation FVIII with co-formulated protein (%)	F %
FVIII (turoctocog alfa/N8) + VWF	2000/0.2 ml/kg	TIL/E/D3/A1	3	99	6.2
N8-GP	700/0.2 ml/kg	—	—	—	40
N8-GP + VWF	700/0.2 ml/kg	TIL/E/D3/A1	3	99	59
N8-GP + VWF	500/1 ml/kg	TIL/E/D3/A1	3	82	34

hindering the passage of FVIII into the bloodstream. Likewise, Hirudin dosed to a level that inhibits thrombin activity in vivo did not affect bioavailability of N8-GP. Thrombin activation of FVIII does thus not appear to affect s.c. FVIII bioavailability.

The antibody 4F30 (further characterised in WO2012035050), which bind to C1 and inhibits cellular uptake of FVIII, did not improve the bioavailability of N8-GP.

The s.c. bioavailability in rabbits of N8-GP and N8-GP co-formulated with VWF fragment TIL/E/D3/A1 dosed in a dosing volume of 0.2 ml/kg was 40 and 59%, respectively. The bioavailability of N8-GP+VWF dosed in a dosing volume of 1 ml/kg was 34%. The bioavailability of N8-GP may thus be influenced either by the species or by the differences in dosing volumes (5 ml/kg in mice and 0.2 ml/kg or 1 ml/kg in rabbits). 0.2 ml/kg is closest to a dosing volume relevant for

humans. FVIII (turoctocog alfa/N8) dosed together with VWF fragment TIL/E/D3/A1 displayed a similar bioavailability in rabbits compared to mice despite the higher dosing concentration.

Example 26

Construction of Expression Vectors Encoding VWF Fragments

Plasmid #796 consisting of the pZEMHygro vector with insert consisting of wild-type human VWF cDNA was utilized as the starting point for generating DNA constructs for the expression of truncated human VWF proteins.

DNA encoding the VWF signal peptide, followed by the VWF TIL/E' domain, the VWF D3 domain, the VWF A1 domain, and a HPC4 tag was generated by polymerase chain reaction (PCR) using plasmid #796 as template, forward primer oLLC089 VWF forward, and reverse primer oLLC092 VWF A1 HPC4 reverse. These primers contain a Nhe I and a Not I restriction site, respectively. The resulting PCR product was inserted into the pCR2.1-TOPO vector (Invitrogen). From here the VWF(TIL/E/D3/A1)-HPC4 coding DNA was excised with the Nhe I and a Not I restriction enzymes and inserted into pZEM219b digested with the same restriction enzymes. Thus, the pLLC089 construct was established consisting of pZEM219b with insert encoding VWF (TIL/E/D3/A1)-HPC4.

Nucleotide substitutions leading to the amino acid replacements C1099/1142S in the VWF VWF(TIL/E/D3/A1)-HPC4 protein encoded by pLLC089 were introduced by site-directed mutagenesis of pLCC089 using the QuikChange XL Site-directed Mutagenesis kit (Stratagene) and the oLLC101-f, oLLC102-r, oLLC103-f, and oLLC104-r mutagenesis primers. The site directed mutagenesis gave rise to the pLLC095 vector consisting of pZEM219b with insert encoding VWF (TIL/E/D3/A1)C1099/1142S-HPC4.

TABLE 9

Oligonucleotide primers used for generating VWF fragment coding DNA constructs	
Primer name	Primer sequence (5'-3')
oLLC089 VWF forward	CCGCTAGCCCATGATTCTGCCAGATTGCGGGTGCTGCTTGCTCTGGCCCTCATTTGCCAGGACCCCTTTGTAGCCTATCTGTGCGGCCCCATG (SEQ ID NO 39)
oLLC092 VWF A1 HPC4 reverse	GATGCGGCGCCTACTACTATTTGCCATCAATCAGACGCGGATCCACCTGATCTTCGGCTTCAGGGCAAGGTACAGAGGTAGC (SEQ ID NO 40)
oLLC101-f	CATTGGGGACTGCGCCTCCTTCTGCGACACCATTGCTGCC (SEQ ID NO 41)
oLLC102-r	GGCAGCAATGGTGTGCGAGAAGGAGGCGCAGTCCCCAATG (SEQ ID NO 42)
oLLC103-f	CGGGAGAACGGGTATGAGTCTGAGTGGCGCTATAACAGCTGTGC (SEQ ID NO 43)
oLLC104-r	GCACAGCTGTTATAGCGCCACTCAGACTCATACCCGTTCTCCCG (SEQ ID NO 44)

Example 27

Stable Cell Lines Expressing VWF Fragments

Baby hamster kidney (BHK) cells grown in Dulbecco's modified Eagle's medium with 10% fetal calf serum were transfected with pLL095 using Genejuice transfection reagent (Merck). A pool of transfected cells was generated by selection with 1.5 M methotrexate giving rise to a non-clonal

BHK cell line producing VWF (TIL/E/D3/A1)C1099/1142S-HPC4. The cells were seeded in a biofermentor and the VWF (TIL/E/D3/A1)C1099/1142S-HPC4 protein was purified from the cell culture supernatant as described in Example 22.

CHO-DUKX-B11 suspension cells grown in suspension were transfected with pLLC095 by electroporation. A pool of transfected cells was generated by adaptation to growth in medium without nucleosides. Subsequently, the pool was adapted to growth in the presence of 100 mM methotrexate giving rise to the VWF (TIL/E/D3/A1)C1099/1142S-HPC4 producing non-clonal CHO-DUKX-B11 cell line MBML001. The cells were seeded in a biofermentor and the VWF (TIL/E/D3/A1)C1099/1142S-HPC4 protein was purified from the cell culture supernatant as described in Example 22.

Example 28

VWF Fragments Protects FVIII Against Cellular Uptake

The effect of plasma-derived (pd) VWF and fragments of VWF on FVIII cellular uptake is evaluated in human monocyte-derived macrophages or dendritic cells, which both are antigen presenting cells, or U87 MG cells. U87 MG cells are obtained from ATCC (HTB-14). The cells are cultured in fibronectin-coated 24-well plates for 48 hours in EMEM supplemented with 10% heat inactivated FCS at 37° C. in 5% CO₂. The cells are carefully washed with buffer A (10 mM HEPES, 150 mM NaCl, 4 KCl, 11 mM Glucose, pH 7.4) and incubated for 15 min with buffer B (buffer A supplemented with 5 mM CaCl₂ and 1 mg/ml BSA). Radioactively labelled FVIII (¹²⁵I-FVIII, final concentration 1 nM) is incubated alone or premixed with different concentrations of pdVWF (American Diagnostica, final concentration 0.001 nM-50 nM based on monomer content) or TIL/E/D3/A1 (final concentration 0.25 nM -500 nM or 1000 nM) 10 min prior to addition

to the U87 MG cells and incubated with the cells 1 hour at 37° C. to allow binding and internalization. Cells are subsequently washed three times with ice-cold buffer B. Surface bound proteins are cleaved off by incubating the cells in PBS containing 100 µg/ml trypsin, 50 µg/ml proteinase K, 5 mM EDTA (pH 7.4) for 1 hour on ice. The detached cells are transferred to tubes and centrifuged to pellet the cells. The supernatant representing the cell bound FVIII is transferred to

new tubes. The radioactivity in tubes with the supernatants (bound FVIII) and cell pellets (internalized FVIII) are quantified in a gamma counter, and values calculated in FVIII concentration by using a standard curve based on ^{125}I -FVIII. Bound ^{125}I -FVIII in the absence of VWF are set to 100%.

Dendritic cells and macrophages are differentiated from monocytes isolated from buffy coats by magnetic separation using magnetic anti-CD14-beads (Miltenyi Biotec) and a MACS column (Miltenyi Biotec) according to the manufacturer's instructions. Monocytes (0.5×10^6 cells/ml) are seeded in T-75 tissue culture flasks and cultured in IMDM media (GIBCO) containing 10% FBS, 1% penicillin/streptomycin and 3.3 ng/ml M-CSF (R&D Systems) in order to differentiate the cells into macrophages. Additional 3.3 ng/ml M-CSF is added after three days of culturing. The monocytes can alternatively be differentiated into dendritic cells by stimulating with 40 ng/ml GM-CSF (R&D Systems) and 40 ng/ml IL-4 for five days. Dendritic cells are washed in buffer B and transferred to low binding Nunc tubes with 0.5×10^6 cells/tube. Fluorescently labelled FVIII, e.g. Oregon-Green FVIII (e.g. 30 and 100 nM) are added and incubated 1 hour at 37° C. Cells are washed once and analysed by flow cytometry using a LRS Fortessa instrument (BD). The macrophages are after six days culturing washed with PBS and incubated 10-20 min at 4° C. with 2.5 mM EDTA in PBS with 5% FCS to detach cells. Macrophages (7×10^5 /well) are seeded on fibronectin-coated 96-well glass bottom tissue culture plates (Perkin Elmer ViewPlate Black). 24 hours post seeding the cells are washed once with buffer B before addition of 30 nM fluorescently-labelled FVIII (e.g. OregonGreen-FVIII) alone or in the presence of increasing concentrations (15-240 nM) of pdVWF (American Diagnostica) or TIL/E/D3/A1. Macrophages are incubated for 1 hour at 37° C. Subsequently, cells are washed twice with buffer B to remove non-internalized material before addition of PBS containing 2.5 µg/ml Hoechst33342 (Molecular Probes) to visualize the cell nuclei. The plate is then immediately imaged on the Operetta® High Content Screening system (Perkin Elmer, Hamburg) in widefield fluorescence mode using the 20× high NA objective. Ten fields per well are imaged and analysed. The approach to image analysis in the Harmony® software is based on counting nuclei (Hoechst channel), followed by texture analysis (FVIII channel) using the "find particle" method to detect vesicular FVIII. Dead or apoptotic cells are excluded from the analysis based on nuclei fragmentation and/or excessive binding of FVIII to the plasma membrane. In order to quantify the internalized FVIII the integrated fluorescent intensity of the vesicular FVIII signal is calculated and plotted against time.

IC50 values for inhibition of FVIII binding and internalization in U87 MG cells and macrophages are shown in table 10. Both pdVWF and TIL/E/D3/A1 are able to inhibit FVIII cell binding/uptake in both cell types providing sufficient high concentrations are used. As uptake in antigen presenting cells is the initial step in presenting FVIII to the immune system, the data may indicate that a reduced immune response can be achieved upon co-formulation of FVIII with a VWF fragment.

TABLE 10

Effect of pdVWF and TIL/E/D3/A1 fragment on FVIII binding and internalization in U87 MG cells and uptake in macrophages.				
Cell type	IC50 (nM)		Maximal inhibition (%)	
	pdVWF	TIL/ E/D3/A1	pdVWF	TIL/ E/D3/A1
U87 (n = 3-4) Binding	1.2 ± 0.9	17.6 ± 13.0	34.3 ± 4.2	39.8 ± 7.8

TABLE 10-continued

Effect of pdVWF and TIL/E/D3/A1 fragment on FVIII binding and internalization in U87 MG cells and uptake in macrophages.				
Cell type	IC50 (nM)		Maximal inhibition (%)	
	pdVWF	TIL/ E/D3/A1	pdVWF	TIL/ E/D3/A1
U87 (n = 3-4) Internalization	1.3 ± 1.2	22.1 ± 19.2	32.2 ± 7.0	41.2 ± 11.5
Macrophages (n = 3)	15.6 ± 3.5	31.5 ± 6.1	32.6 ± 11.4	47.2 ± 11.7

Example 29

Efficacy of FVIII Compounds Co-Formulated with VWF Variants after Subcutaneous Dosing:

FVIII deficient, FVIII-KO mice, 12-16 weeks old, male and females are divided into 3 groups of 12 animals. In each group, eight animals are subjected to tail bleeding and 4 animals are used in parallel for ex vivo efficacy testing using ROTEM analysis.

GlycoPEGylated FVIII or vehicle is dosed s.c. 24 hr prior to tail transection. As a positive control glycoPEGylated FVIII is dosed i.v. 5 min prior to injury. The s.c injection is performed in the neck and the i.v. injection in a lateral tail vein. The dose volume is 5 ml/kg.

GlycoPEGylated FVIII is prepared in buffer (10 mM L-Histidine, 8.8 mM Sucrose, 0.01% Polysorbate 80, 308 mM NaCl, 1.7 mM CaCl₂ (dihydrate), 0.01% Polysorbate 80 0.1 mg/ml, pH 6.9) to a concentration of 40 and 500 IU/ml and stored at -80° C. until use.

Before tail transection, the mice are anaesthetised with isoflurane and placed on a heating pad. The tails are placed in pre-heated saline at 37° C. for 10 min. The tail is transected 4 mm from the tip.

Immediately before tail transection a 20 µl blood sample is drawn from the peri-orbital plexus for FVIII determination.

Blood is collected over 30 min and the haemoglobin concentration determined by spectrophotometry at 550 nm.

Parallel animals are used for blood sampling and subsequent analysis of their clotting parameters (ex vivo efficacy). A blood sample is taken from the peri-orbital plexus with 20 µL capillary tubes without additive. The blood sample is diluted 1:10 in 0.13M sodium citrate and carefully mixed and stored at room temperature for immediate thromboelastography by ROTEM. The blood sample is re-calcified by adding 7 µL CaCl₂ to a mini curvet (StarTEM). Thereafter, 105 µL of blood is added to the mini curvet and mixed. The analysis is performed until the maximum amplitude is reached.

Results:

The prophylactic effect of s.c. administered FVIII is determined by comparing the blood loss during the 30 min study period at 24 hr after s.c. administration to that of 1) a vehicle control group and 2) an i.v. control group with glycoPEGylated FVIII. The blood loss in the group dosed s.c. with glycoPEGylated FVIII is comparable to the blood loss in the group dosed i.v. (FIG. 10, left panel). The blood loss data are supported by the ex vivo efficacy parallel study of the examined clotting parameters, e.g. clot time (FIG. 10, right panel).

In conclusion, subcutaneously administered FVIII appear to be hemostatically active based on the PK profile and the results from the ex vivo activity. Therefore, subcutaneously administered FVIII co-formulated with a VWF fragment is

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also believed to be hemostatically active as can be predicted from its pharmacokinetic profile.

Example 30

Effect of s.c. Administered FVIII±VWF Fragments in FVIII-Deficient Mice.

Test Compounds: Test compounds are prepared in 10 mM L-Histidine (1.55 mg/ml), 8.8 mM Sucrose (3.0 mg/ml), 308 mM NaCl (18 mg/ml), 1.7 mM CaCl₂ dihydrate (0.25 mg/ml), 0.01% Polysorbate 80 (0.1 mg/ml), pH 7.3.

Animals: Experiments are performed using groups of F8 knockout (FVIII k/o) mice (129/C57BL/6 or C57BL/6, exon 16 disrupted). Animals are included in experiments when 12-18 weeks old at which time they are weighing roughly 18-25 grams. Twelve to 15 animals are included per group.

Administration of test compounds: Test compounds are administered subcutaneously (or intravenously for controls) using a dose volume of maximally 10 ml/kg (or 5 ml/kg for controls).

Bleeding Model: A tail vein transection (TVT) bleeding model is conducted with the mice under full isoflurane anaesthesia. Briefly, following anaesthesia the bleeding challenge comprises a template-guided transection of a lateral tail vein at a tail diameter of 2.7 mm. The tail is immersed in saline at 37° C. allowing visual recording of the bleeding for 60 min, where after the blood is isolated and the blood loss determined by measuring the haemoglobin concentration as described in "Example 3". When feasible and justified, blood is sampled for assessment of FVIII activity (FVIII:C) in plasma as described above.

Dose Response: Different doses of FVIII or FVIII co-formulated with VWF fragments (e.g. N8-GP/VWF) are injected subcutaneously at defined time point(s) prior to TVT. Vehicle and intravenous control/treatment groups are included for no effect and maximal effect, respectively.

Duration of Action: FVIII or FVIII/VWF is injected s.c. to identify prolonged effect, i.e. improved bleeding phenotype after treatment. TVT is performed at several time points, e.g. 24, 48, 72, 96, after dosing.

Repeated Dose: FVIII or FVIII/VWF fragment is dosed s.c. once daily for several days. TVT is performed at different time points to assess any improvement in the bleeding phenotype.

Data Processing and Analyses: Data are physically recorded throughout the experiment. Hereafter, data are aggregated for analysis using MS Excel (Microsoft, Wash., USA) before being analysed in GraphPad Prism version 5 (GraphPad Software, Inc, CA, USA).

Example 31

Effect of s.c. FVIII±VWF Fragments in Other FVIII-Deficient Species.

Additional pharmacodynamic experiments are conducted in other species to verify effect after subcutaneous administration in non-murine animal models of haemophilia A, e.g. rat and dog. FVIII or FVIII/VWF are injected subcutaneously before assessing ex vivo effect, before inducing a bleeding challenge, or as a means to treat or prevent spontaneous bleeds.

Test Compounds: Test compounds are prepared in 10 mM L-Histidine (1.55 mg/ml), 8.8 mM Sucrose (3.0 mg/ml), 308 mM NaCl (18 mg/ml), 1.7 mM CaCl₂ dihydrate (0.25 mg/ml), 0.01% Polysorbate 80 (0.1 mg/ml), pH 7.3.

Animals: Experiments are performed in adolescent rats (~12 weeks old) or dogs (6+ months old) with haemophilia A.

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Administration of test compounds: Test compounds are administered subcutaneously (or intravenously for controls) using a dose volume of maximally 10 ml/kg (or 5 ml/kg for controls).

5 Dog effect model: In dogs with haemophilia A the effect is assessed ex vivo using surrogate markers, e.g. thrombelastography as previously described (Knudsen et al, 2011; Haemophilia, 17, 962-970), or in vivo, e.g. using a standardized bleeding challenge monitored by acoustic force radiation force impulse (ARFI) ultrasound as described (Scola et al, 2011; Ultrasound in Med. & Biol., 37(12), 2126-2132). Capacity allowing, test compound are administered to treat spontaneously bleeding dogs. Effect is monitored by assessing the resolution of clinical manifestation in comparison with historic data on i.v. treatment.

15 Rat effect model: In rats with haemophilia A the effect is assessed ex vivo using surrogate markers, e.g. thrombelastography as described above for mice and dogs, or in vivo, e.g. using a standardized bleeding challenge as described for mice. Capacity allowing, test compound are administered to treat spontaneously bleeding rats. Effect is monitored by assessing the resolution of clinical manifestation in comparison with historic data on i.v. treatment.

20 Additional pharmacodynamic experiments are conducted in other species to verify effect after subcutaneous administration in non-murine animal models of haemophilia A, e.g. rat and dog.

Example 32

Construction of Expression Vectors Encoding VWF Fragments

A nucleotide substitution leading to the amino acid replacement S1142C in the VWF(764-1250)-C1099/1142S-ALA-HPC4 protein encoded by pJSV348 described in Example 17 was introduced by PCR-based site-directed mutagenesis using the VWF 1099C S and VWF 1099C AS primers (Table P). This gave rise to the pGB237 vector consisting of pTT5 with insert encoding VWF(764-1250)-C1099S-ALA-HPC4 (SEQ ID NO 11). The cysteine at position 1142 allows dimerization of the protein as described in Example 20.

40 Likewise, a nucleotide substitution leading to the amino acid replacement S1099C in the VWF(764-1250)-C1099/1142S-ALA-HPC4 protein encoded by pJSV348 described in Example 17 was introduced by PCR-based site-directed mutagenesis using the VWF 1142C S and VWF 1142C AS primers (Table P). This gave rise to the pGB238 vector consisting of pTT5 with insert encoding VWF(764-1250)-C1142S-ALA-HPC4 (SEQ ID NO 11). The cysteine at position 1099 allows dimerization of the protein as described in Example 20.

In a similar manner, the S1099C amino acid replacement was introduced in the VWF(764-1128)-C1099S-HPC4 protein encoded by pJSV406 described in Example 18, giving rise to the pGB249 vector consisting of pTT5 with insert encoding VWF(764-1128)-HPC4 (SEQ ID NO 9). The cysteine at position 1099 allows dimerization of the protein as described in Example 20.

60 cDNA encoding amino acid 1-1250 of human VWF was amplified by PCR using plasmid #796 (described in Example 26) as template, forward primer JP1000 VWF-HindIII S (Table 2), and reverse primer JP1006 VWF764-1250 (Table 2). Primer JP1006 VWF764-1250 contains a Nhe I site. The resulting PCR product was inserted into the pCR4BLUNT-TOPO vector (Invitrogen) downstream of Pme I restriction site. From here, the vWF(1-1250) coding DNA was excised

with the Pme I and a Nhe I restriction enzymes and inserted into pJSV164 described in Example 17 generating the pGB242 vector consisting of pTT5 with insert encoding vWF (1-1250)-ALA-HPC4. The cysteines at position 1099 and 1142 allow dimerization of the protein as described in Example 20, and proteolytic removal of the presequence will generate vWF(764-1250)-ALA-HPC4 (SEQ ID NO 11).

DNA sequences of pJSV348 (described in Example 17) and construct #796 (described in Example 26) were inverse amplified by PCR using overlapping primers. The pJSV348 sequence was amplified using primer 2764pJSV348 and 1202pJSV348R (Table P), while the construct #796 sequence was amplified using primer 221#796F and 3537#796R (Table P). The amplification products from pJSV348 (recipient) and construct #796 (donor) were excised from an agarose gel and joined by ligation independent cloning (LIC) using the In-Fusion HD Cloning Kit (Clontech) to generate circular DNA and subsequently transformed into Stellar competent cells (Clontech). The resulting expression vector, named pGB252 consists of PTT5 with insert encoding VWF(1-1128)-ALA-HPC4. The cystein at position 1099 allows dimerization of the protein as described in Example 20, and proteolytic removal of the presequence will generate vWF(764-1128)-ALA-HPC4 (SEQ ID NO 9).

Likewise, amplification using pJSV348 (described in Example 17) as template with the primers 2764pJSV348 and 1202pJSV348R (Table P) and amplification using #796 (described in Example 26) as template with the primers 221#796F and 3747#796R (Table P) generated pJSV348 (recipient) and construct #796 (donor) amplification products that were also excised from an agarose gel and joined by

ligation independent cloning (LIC) using the In-Fusion HD Cloning Kit (Clontech) to generate circular DNA and subsequently transformed into Stellar competent cells (Clontech). The resulting expression vector, named pGB253 consists of PTT5 with insert encoding VWF(1-1198)-ALA-HPC4. The cysteines at position 1099 and 1142 allow dimerization of the protein as described in Example 20, and proteolytic removal of the presequence will generate vWF(764-1198)-ALA-HPC4 (SEQ ID NO 10).

In a similar manner, DNA sequences of pJSV348 (described in Example 17) and construct #796 (described in Example 26) were inverse amplified by PCR using overlapping primers. The pJSV348 sequence was amplified using primer 2764pJSV348 and 2420pJSV348R (Table 11), while the construct #796 sequence was amplified using primer 3666#796F and 5203#796R (Table P). The amplification products from pJSV348 (recipient) and construct #796 (donor) were excised from an agarose gel and joined by ligation independent cloning (LIC) using the In-Fusion HD Cloning Kit (Clontech) to generate circular DNA and subsequently transformed into Stellar competent cells (Clontech). The resulting expression vector, named pGB250 consists of PTT5 with insert encoding VWF(764-1873)-C1099/1142C-ALA-HPC4 (SEQ ID NO 20).

Human VWF cDNA sequences amplified from construct #796 (described in Example 26) were combined generating the pLLC122 vector consisting of pZEM219b with insert encoding vWF (1-1464)-HPC4. The cysteines at position 1099 and 1142 allow dimerization of the protein as described in Example 20, and proteolytic removal of the presequence will generate vWF(764-1464)-HPC4 (SEQ ID NO 19).

TABLE 11

Oligonucleotide primers used for generating VWF fragment coding DNA constructs	
Primer name	Primer sequence (5'-3')
VWF 1099C S	GGGGACTGCGCTGCTTCTGCGACACC (SEQ ID NO 45)
VWF 1099C AS	GGTGTGCGCAGAAGCAGGCGCAGTCCCC (SEQ ID NO 46)
VWF 1142C S	GAACGGGTATGAGTGTGAGTGGCGCTATA (SEQ ID NO 47)
VWF 1142C AS	TATAGCGCCACTCACACTCATACCCGTTT (SEQ ID NO 48)
2764pJSV348F	GCGCTAGCTGAGGACCAAGTAGATCCGCGGCTCATTGATGGG (SEQ ID NO 49)
1202pJSV348R	GGGCCAGAGCAAGCAGCACCCCGCAAATCTGGCAGG (SEQ ID NO 50)
221#796F	CCTGCCAGATTTGCCGGGTGCTGCTTGCTCTGGCCC (SEQ ID NO 51)
3537#796R	TACTTGGTCCTCAGCTAGCGCCTGGGGGCACAATGTGGCGTCCTCC (SEQ ID NO 52)
3747#796R	TACTTGGTCCTCAGCTAGCGCCACTGGACAGTCTTCAGGGTCAACGC (SEQ ID NO 53)
2420pJSV348R	GGCTCAGGGTGCTGACACGTGACTTGACAGGCAGGTGC (SEQ ID NO 54)
3666#796F	GCACCTGCCTGTCAAGTCACGTGTCAGCACCCCTGAGCC (SEQ ID NO 55)
5203#796R	TACTTGGTCCTCAGCTAGCGCTGCAGGGGAGAGGGTGGGATCTGC (SEQ ID NO 56)

VWF Fragments Inhibit FVIII Uptake by Human Dendritic Cells.

Human monocyte-derived dendritic cells were prepared as described in example 28. Expression of the dendritic cell markers CD209 and CD86 were controlled by flow cytometry using a LRS Fortessa instrument (BD). Fluorescent labelled FVIII (Oregon green-FVIII, 30 nM final concentration) was premixed with different concentrations of plasma-derived VWF or VWF fragments before incubating 1 h at 37° C. with dendritic cells. Live/Dead cell kit (Invitrogen #L10119, APC-Cy7) was used for gating on live dendritic cells, and FVIII uptake within this cell population was quantified. Data was normalized for each individual experiment. The signal in samples without VWF was defined as 100% FVIII uptake, and the signal in the sample with the highest concentration of plasma-derived VWF (240 nM based on monomer content) was defined as 0%. Values from 3-5 experiments were combined and IC50 values calculated using non-linear regression in Prism software (log(inhibitor) vs. response—Variable slope (four parameters)). The resulting IC50 values are shown in table 12. The data show that all tested VWF fragments were able to inhibit FVIII uptake by the dendritic cells provided sufficiently high concentrations are used. As FVIII uptake by antigen-presenting cells is the initial step in presenting FVIII to the immune system the data suggests that co-formulation of FVIII with sufficiently high concentration of VWF fragment may have a potential in reducing immunogenicity of FVIII.

TABLE 12

Effect of plasma derived VWF and VWF fragments on FVIII uptake in dendritic cells.		
Domain/comment	VWF fragment sequence	IC50 (nM)*
TIL'/E'/VWD3	VWF(764-1041)-ALA-HPC4 monomer	570 (400-820)
TIL'/E'/D3	VWF(764-1250)-C1099/1142S-ALA-HPC4 monomer	31 (25-39)
TIL'E/D3/A1 monomer	VWF(764-1464)-C1099/1142S-HPC4 monomer	31 (18-52)
TIL'E/D3/A1 dimer	VWF(764-1464)-HPC4 dimer**	16 (11-22)
Plasma-derived VWF	VWF (764-2813)	9.8 (7.6-13)

*Best fit value and 95% confidence intervals of data from 3-5 experiments

**IC50 value based on molar concentration of the dimer, i.e. multiply IC50 with 2 to reflect IC50 value based on content of VWF monomer fragment.

Effect of s.c. FVIII±VWF Fragments in Animals with Inhibiting Antibodies Against FVIII.

The objective is to evaluate the potential of pharmaceutical compositions to treat haemophilia A patients with inhibitors against FVIII. We dose FVIII alone or co-formulated with VWF-fragments subcutaneously to naïve FVIII-KO mice or FVIII-KO mice where inhibitors are induced by repeated subcutaneous or intravenous administrations of FVIII prior to treatment with the compositions, or by injecting a polyclonal or monoclonal anti-FVIII antibody. The effect of the treatments is evaluated in anaesthetized mice after transection of a lateral tail vein. The tail is placed in pre-warmed saline at 37° C. and the bleeding is observed for 60 minutes. The blood loss during the experiment is a measure of the effect of the composition.

Administration of VWF Fragments to VWF Knockout Mice:

Test Compound:

Murine VWF Fragment TIL'/E'/D3/A1 1.829 nmol/ml, 0.015 mg/ml

The test compound was formulated in 20 mM imidazol 150 mM NaCl, 0.02% Tween 80, 1.1M Glycerol, 10 mM CaCl2, pH 7.3

6 VWF knockout mice, with an approximate weight of 25 g were dosed intravenously in the tail with 9.48 nmol/kg Murine VWF fragment TIL'/E'/D3/A1.

Blood was sampled pre-dose and at 0.08, 0.33, 0.5, 1, 2, 4, 7, 18 and 24 h post administration in a sparse sample design with 2 mice sampled per time point. The mice were anaesthetized by Isoflurane/O2/N2O prior to blood sampling via the retroorbital plexus. Three samples were taken from each mouse. Blood (45 µl) was stabilised with 5 µl of sodium-citrate (0.13 M) and added 200 µl FVIII coatest SP buffer (50 mM TRIS-HCl, 1% BSA, Ciprofloxacin 10 mg/L, pH 7.3). After centrifugation at 4000 g for 5 minutes at room temperature, the supernatants were immediately frozen on dry ice before storage at -80° C. prior to analysis.

Samples were analysed with regards to FVIII concentration in an antigen LOCI assay (Luminescence oxygen channeling immunoassay).

Mean plasma concentration versus time data were analysed relatively to the predose values.

The relative mean FVIII concentration in time after dosing is shown in table 13

TABLE 13

Effect of Murine D'D3A1 IV on FVIII blood concentration in VWF KO mice.		
	Time (h)	FVIII increase (% of predose)
	0.08	174
	0.33	190
	0.5	176
	1	163
	2	274
	4	250
	7	330
	18	225
	24	207

FVIII concentration increased gradually in time after dosing of VWF fragment intravenously with a Tmax after 7

hours. This finding supports the potential for VWF fragments for the treatment of VWF disease as well as haemophilic disorders.

Example 36

Interaction Mapping by HX-MS of vWF Fragments TIL'/E'/D3/A1, TIL'/E'/D3, TIL'E, and TIL'/E'/VWD3 on Turoctocog Alfa (FVIII) and Turoctocog Alfa (FVIII) on vWF Fragment TIL'/E'/D3/A1

Introduction to HX-MS

The HX-MS technology exploits that hydrogen exchange (HX) of a protein can readily be followed by mass spectrometry (MS). By replacing the aqueous solvent containing hydrogen with aqueous solvent containing deuterium, incorporation of a deuterium atom at a given site in a protein will give rise to an increase in mass of 1 Da. This mass increase can be monitored as a function of time by mass spectrometry in quenched samples of the exchange reaction. The deuterium labelling information can be sub-localized to regions in the protein by pepsin digestion under quench conditions and following the mass increase of the resulting peptides.

One use of HX-MS is to probe for sites involved in molecular interactions by identifying regions of reduced hydrogen exchange upon protein-protein complex formation. Usually, binding interfaces will be revealed by marked reductions in hydrogen exchange due to steric exclusion of solvent. Protein-protein complex formation may be detected by HX-MS simply by measuring the total amount of deuterium incorporated in either protein members in the presence and absence of the respective binding partner as a function of time. The HX-MS technique uses the native components, i.e., protein and antibody or Fab fragment, and is performed in solution. Thus HX-MS provides the possibility for mimicking the in vivo conditions (for a recent review on the HX-MS technology, see Wales and Engen, *Mass Spectrom. Rev.* 25, 158 (2006)).

Materials

Protein batches used were:

FVIII protein batches used were:

FVIII (N8, Turoctocog alfa, SEQ ID NO 2) Batch 0155-0000-0004-37A

vWF Fragments

D'D3A1 (SEQ ID NO 19; Cys1099Ser; Cys1142Ser) Batch 0129-0000-0170-6B; 2304 (SEQ ID NO 5) Batch 0129-0000-2304-1B; 2307 (SEQ ID NO 8) Batch 0129-0000-2307-1B; 2308 (SEQ ID NO 11) Batch 0129-0000-2308 2B.

All proteins were buffer exchanged into 20 mM Imidazole, 500 mM NaCl, 10 mM CaCl₂, adjusted to pH 7.3 before experiments.

Methods: HX-MS Experiments

Instrumentation and Data Recording

The HX experiments were performed on a nanoACQUITY UPLC System with HDX Technology (Waters Inc.) coupled to a Synapt G2 mass spectrometer (Waters Inc.). The Waters HDX system contained a Leap robot (H/D-x PAL; Waters Inc.) operated by the LeapShell software (Leap Technologies Inc./Waters Inc.), which performed initiation of the deuterium exchange reaction, reaction time control, quench reaction, injection onto the UPLC system and digestion time control. The Leap robot was equipped with two temperature controlled stacks maintained at 20° C. for buffer storage and HX reactions and maintained at 2° C. for storage of protein and quench solution, respectively. The Waters HDX system furthermore contained a temperature controlled chamber holding the pre- and analytical columns, and the LC tubing and

switching valves at 1° C. A separately temperature controlled chamber holds the pepsin column at 25° C. For the inline pepsin digestion, 100 µL quenched sample containing 100 pmol hIL-21 was loaded and passed over a Poroszyme® Immobilized Pepsin Cartridge (2.1×30 mm (Applied Biosystems)) placed at 25° C. using a isocratic flow rate of 100 µL/min (0.1% formic acid:CH₃CN 95:5). The resulting peptides were trapped and desalted on a VanGuard pre-column BEH C18 1.7 µm (2.1×5 mm (Waters Inc.)). Subsequently, the valves were switched to place the pre-column in-line with the analytical column, UPLC-BEH C18 1.7 µm (1×100 mm (Waters Inc.)), and the peptides separated using a 8 min gradient of 8-45% B delivered at 120 µL/min from the nanoACQUITY UPLC system (Waters Inc.). The mobile phases consisted of A: 0.1% formic acid and B: 0.1% formic acid in CH₃CN. The ESI MS data and the separate elevated energy (MS^E) experiments were acquired in positive ion mode using a Synapt G2 mass spectrometer (Waters Inc.). Leucine-enkephalin was used as the lock mass ([M+H]⁺ ion at m/z 556.2771) and data was collected in continuum mode (For further description, see Andersen and Faber, *Int. J. Mass Spec.*, 302, 139-148 (2011)).

Data Analysis

Peptic peptides were identified in separate experiments using standard MS^E methods where the peptides and fragments are further aligned utilizing the ion mobility properties of the Synapt G2 (Waters Inc.). MS^E data were processed using ProteinLynx Global Server version 2.5 (Waters Inc.). The HX-MS raw data files were processed in the DynamX software (Waters Inc.). DynamX automatically performs the lock mass-correction and deuterium incorporation determination, i.e., centroid determination of deuterated peptides. Furthermore, all peptides were inspected manually to ensure correct peak and deuteration assignment by the software.

Epitope Mapping Experiment

Amide hydrogen/deuterium exchange (HX) was initiated by a 10-fold dilution of FVIII in the presence or absence of vWF fragment, i.e., D'D3A1, 2308, 2307, or -2304 at time 0 into 20 mM Imidazole, 150 mM NaCl, 10 mM CaCl₂, pH 7.3 (uncorrected value) at later time points into the corresponding deuterated buffer (i.e. 20 mM Imidazole, 150 mM NaCl, 10 mM CaCl₂ prepared in D₂O, 98% D₂O final, pH 7.3 (uncorrected value)). All HX reactions were carried out at 20° C. and contained 3 µM FVIII in the absence or presence of 4.5 µM vWF fragment thus giving a 1.5 fold molar excess of vWF fragment binding partner. At appropriate time intervals ranging from 10 sec to 240 sec, 50 µL aliquots of the HX reaction were quenched by 50 µL ice-cold quenching buffer (1.36 M TCEP, 2 M urea) resulting in a final pH of 2.5 (uncorrected value).

Results and Discussion

Interaction Mapping of 2304 and 2307 on FVIII

The HX time-course of 191 peptides, covering 83% of the primary sequence of FVIII were monitored in the absence or presence of the vWF fragments 2304 or 2307 for i.e., 10, 20, 30, 40, 60, 120, and 240 sec.

The vWF fragments 2304 and 2307 both induce identical alterations in the exchange profile of FVIII and will be described together here. The observed exchange pattern in the time points (i.e., 10, 20, 30, 40, 60, 120, and 240 sec) in the presence or absence of 2304/2307 can be divided into different groups: One group of peptides display an exchange pattern that is unaffected by the binding of 2304/2307. In contrast, another group of peptides in FVIII show protection from exchange upon 2304/2307 binding.

The regions displaying protection upon 2304/2307 binding encompass peptides covering residues 1855-1875, 1857-1875, 2062-2070, 2125-2147, 2125-2148, 2127-2147, 2275-2291, 2275-2302, 2275-2305, 2292-2305, and 2293-2312 (Table 14). However, by comparing the relative amounts of exchange protection within each peptide upon binding 2304/2307 and the lack of epitope effects in overlapping and adjacent peptides in these regions, the regions that display reduced deuterium incorporation can be narrowed to residues 1862-1875, 2062-2070, 2125-2147, and 2285-2299.

Interaction Mapping of D'D3A1 and 2308 on FVIII

The HX time-course of 185 peptides, covering 79% of the primary sequence of FVIII were monitored in the absence or presence of the vWF fragments D'D3A1 or 2308 for 10, 20, 30, 40, 60, 120, and 240 sec.

The vWF fragments D'D3A1 and 2308 both induce identical alterations in the exchange profile of FVIII and will be described together here.

The regions displaying protection upon D'D3A1 or 2308 binding encompass peptides covering residues 1669-1680, 1738-1765, 1743-1765, 1856-1869, 1870-1874, 2061-2074, 2063-2074, 2123-2146, and 2260-2280 (Table 15).

However, by comparing the relative amounts of exchange protection within each peptide upon binding of D'D3A1 or 2308 and the lack of epitope effects in overlapping and adjacent peptides in these regions, the regions that display reduced deuterium incorporation can be narrowed to residues 1671-1680, 1745-1754, 1858-1874, 2063-2074, 2125-2146, 2262-2280.

Interaction Mapping of FVIII on D'D3A1

The HX time-course of 82 peptides, covering 58% of the primary sequence of vWF fragment D'D3A1 were monitored in the absence or presence of FVIII for 10, 20, 40, 60, 120, and 240 sec.

The region displaying exchange protection upon FVIII binding encompass the peptide covering residues 768-778 (Table 16).

However, by comparing the relative amounts of exchange protection within each peptide upon binding FVIII and the lack of epitope effects in overlapping and adjacent peptides in these regions, the regions that display reduced deuterium incorporation can be narrowed to residues 770-778.

Conclusion

Upon binding of either 2304 or 2307 all regions of FVIII showed similar responses. The same group of peptides were affected by vWF fragment binding in the early time-points.

Furthermore, these affected regions identified for 2304/2307 binding were found to show overlap with affected regions upon binding to D'D3A1/2308 within domain A3 and C1 of FVIII.

Due to lacking sequence coverage of the peptic peptide map conducted to the HX-MS time course of 2304/2307 binding it was not possible to exchange characteristics for residues 1671-1680. Thus it was not possible to verify if 2304/2307 binding induces exchange protection to this region as it was identified upon D'D3A1/2308 binding.

Upon binding of FVIII the regions covering residues 770-778 of D'D3A1 showed exchange protection. The obtained sequence coverage of 58% of D'D3A1 afforded by the peptic peptides conducted to HXMS analysis of FVIII binding, does not allow to leave out that more interaction site are present within D'D3A1/2308.

Conclusion

The identified regions of FVIII showing protection upon binding to vWF fragments D'D3A1, 2308, 2304, or 2307 are structurally situated at remote distances when mapping on to the crystal structure PDB: 2R7E. This makes it highly

unlikely that they can all be assigned to protection induced by binding interface between FVIII and the vWF fragments D'D3A1, 2308, 2304, or 2307. The HX-MS analysis is unable to distinguish between exchange protection induced by binding interface with exchange protections induced by rapid conformational changes.

Thus it is plausible that the observed regions showing exchange protection upon binding to vWF fragments D'D3A1, 2308, 2304, or 2307 are induced by both binding interface and conformational changes of FVIII.

The HXMS study of FVIII binding to vWF fragments D'D3A1, 2308, 2304, or 2307 revealed overlapping regions within domains A3 and C1, and therefore the complex binding to this part of FVIII is identical for the vWF fragments investigated.

The observed discrepancy in domain C2 hints that this part of FVIII undergoes conformational changes upon complex formation with the vWF-fragments. Furthermore, the obtained results hint that the truncation differences between D'D3A1/2308 and 2304/2307 induces different conformational changes of domain C2. In contrast the truncation difference between 2304 and 2307 does not seem to affect the conformational orientation of C2, since identical exchange profiles of domain C2 were observed for binding to these vWF-fragment species.

It is well known that the domains C1 and C2 are essential for the membrane binding affinity of FVIII. It can be speculated that conformational changes of these part of FVIII will reduce the membrane binding ability of FVIII. The conformational position of domains C1 and C2 of FVIII complex bound to the vWF fragments might be unfavourable for membrane binding affinity of FVIII. Furthermore, it is highly likely that the fragments in complex with FVIII will shield for the membrane binding affinity of FVIII as it has been established for the membrane binding characteristics of FVIII complex bound to endogenous vWF. A reduced membrane binding affinity of FVIII complex bound to the vWF fragments in comparison to free FVIII would lead to a reduced binding of FVIII to cell membranes of the immune system, e.g. antigen presenting cells. This could decrease presentation of FVIII-derived peptides on MHC class II and it can therefore be speculated that FVIII complex bound to vWF fragments will be less immunogenic than free FVIII.

TABLE 14

HXMS analysis of FVIII (Turoctocog alfa; seq. no. using wt FVIII) (SEQ ID 2) binding to the vWF fragments 2304 (SEQ ID 5) or 2307 (SEQ ID 8). After deuterium exchange reaction, FVIII is digested with pepsin yielding the present peptic peptides identified to show exchange protection in the presence of 2304 or 2307.				
Sequence	Domain	2304	2307	
L1855-E1875	A3	EX	EX	
V1857-E1875	A3	EX	EX	
W2062-W2070	A3	EX	EX	
V2125-R2147	C1	EX	EX	
V2125-Y2148	C1	EX	EX	
F2127-R2147	C1	EX	EX	
F2275-T2291	C2	EX	EX	
F2275-L2302	C2	EX	EX	
F2275-Y2305	C2	EX	EX	
P2292-Y2305	C2	EX	EX	
V2293-S2312	C2	EX	EX	

EX: exchange protection of FVIII residues upon 2304 or 2307 binding indicating interaction region (40 sec incubation in D2O, >0.4 Da).

TABLE 15

HXMS analysis of FVIII (Turoctocog alfa; seq. no. using wt FVIII) (SEQ ID 2) binding to the vWF fragments D'D3A1 (SEQ ID 19; Cys1099Ser; Cys1142Ser) or 2308 (SEQ ID 11; Cys1099Ser; Cys1142Ser). After deuterium exchange reaction, FVIII is digested with pepsin yielding the present peptic peptides identified to show exchange protection in the presence of D'D3A1 or 2308.			
Sequence	Domain	D'D3A1	2308
S1669-Y1680	a3	EX	EX
F1738-E1765	A3	EX	EX
F1743-E1765	A3	EX	EX
L1856-R1869	A3	EX	EX
Q1870-Q1874	A3	EX	EX
A2061-D2074	C1	EX	EX
S2063-D2074	C1	EX	EX
L2123-A2146	C1	EX	EX
F2260-V2280	C2	EX	EX

EX: exchange protection of FVIII residues upon D'D3A1 or 2308 binding indicating interaction region (40 sec incubation in D2O, >0.4 Da).

TABLE 16

HXMS analysis of vWF fragment D'D3A1 (SEQ ID 19; Cys1099Ser; Cys1142Ser) binding to the FVIII (Turoctocog alfa (SEQ ID 2). After deuterium exchange reaction, D'D3A1 is digested with pepsin yielding the present peptic peptide identified to show exchange protection in the presence of FVIII.		
Sequence	Domain	FVIII
R768-A778	D'	EX

EX: exchange protection of D'D3A1 residues upon FVIII binding indicating interaction region (40 sec incubation in D2O, >0.4 Da).

Example 37

Complex Formation of FVIII (SEQ ID 2) with TIL'/E'/D3/A1 III (SEQ ID 19; Cys1099Ser; Cys1142Ser) and of FVIII (SEQ ID 2) with TIL'/E'/D3 II (SEQ ID 14; Cys1099Ser; Cys1142Ser) Analysed by SEC-UV.

Materials

Protein Batches Used were:

FVIII Protein Batches Used were:

FVIII (N8, Turoctocog alfa, SEQ ID NO 2) Batch 0155-0000-0004-37A; TIL'/E'/D3/A1 III (SEQ ID NO 19; Cys1099Ser; Cys1142Ser) Batch 0129-0000-0170-6B; TIL'/E'/D3 II (SEQ ID 14; Cys1099Ser; Cys1142Ser) Batch 0129-0000-2309-1B.

Methods

Size-exclusion chromatography was performed on a Waters Biosuite 4.6x300 mm column using a flow rate of 0.3 ml/min and a running buffer of 155 mM NaCl, 10 mM Calciumacetat, 10% Isopropanol at 25° C. The absorbance of the effluent was monitored by a UV detector at 280 nm. SEC-UV characterization were performed of FVIII, TIL'/E'/D3/A1 III, TIL'/E'/D3 II, and 1:2 complexes of FVIII—TIL'/E'/D3/A1 III and of FVIII—TIL'/E'/D3 II. Samples of FVIII 10 µM, TIL'/E'/D3/A1 III 20 µM, TIL'/E'/D3 II 20 µM, and in complex were prepared and 15 µL were loaded on to the column.

Results and Conclusion

SEC-UV of the mixtures of FVIII—TIL'/E'/D3/A1 III and FVIII—TIL'/E'/D3 II showed significant fractions of the complex to elute intact from the column. The complex would be expected to elute a little earlier than FVIII; this was also observed in both cases.

Example 38

Preparation of Dimer Form of VWF Fragment: 764-1242 (SEQ ID NO 57) and 764-1482 (SEQ ID NO 58)

In the native full length VWF molecule (SEQ ID NO 22) two cysteine residues in the N-terminal part of the molecule are supposed to participate in the dimerization/multimerization of VWF: Cys1099 and Cys1142.

In some cases, a dimeric form of the VWF fragments is wanted. This can be accomplished in several ways:

One method to accomplish dimer formation is to keep the two residues at position 1099 and position 1142 as cysteines. In order to make a recombinant dimeric molecule, the cDNA encoding the desired VWF fragment is including the pre-sequence of VWF e.g. the D1D2 sequence of VWF (amino acid residues 23-763 of SEQ ID NO 22). This will, during synthesis in the golgi apparatus align two monomers of a given VWF fragment in a configuration allowing a dimeric molecule to be formed with two disulphide bonds in which Cys1099 in monomer 1 is connected to a Cys1099 in monomer 2 and Cys1142 in monomer 1 is connected to Cys1142 in monomer 2. The pre-sequence is cleaved of during secretion of the dimeric VWF protein.

Another method to accomplish dimer formation is to avoid the inclusion of the pre-sequence (amino acid residues 23-763 of SEQ ID NO 22) and simply let a recombinant VWF fragment with Cys in position 1099 and 1142 form a dimeric molecule. This can in principle result in a series of different dimers e.g.:

Cys1099-Cys1099/Cys1142-Cys1142 (two disulphide bonds—like above)

Cys1099-Cys1142/Cys1099-Cys1142 (two disulphide bonds)

Cys1099-Cys1099 (one disulphide bond)

Cys1142-Cys1142 (one disulphide bond)

Cys1099-Cys1142 (one disulphide bond)

Yet another method to accomplish dimer formation is to replace one of the cysteine residues 1099 or 1142 with other amino acid residues (e.g. Serine, Arginine).

If Cys1099 is replaced with a non-Cysteine residue, the molecule can form a dimer by establishment of a disulphide bond between Cys1142 in monomer 1 with Cys1142 in monomer 2.

If Cys1142 is replaced with a non-Cysteine residue, the molecule can form a dimer by establishment of a disulphide bond between Cys1099 in monomer 1 with Cys1099 in monomer 2.

The dimeric forms mentioned above are constructed either with or without the D1D2 pre-sequence of VWF (amino acid residues 23-763 of SEQ ID NO 22).

The different monomeric and dimeric forms will have different properties with regards to their binding to FVIII, their ease of production and their effect on bioavailability of FVIII when injected subcutaneously as a co-formulation.

Example 39

Purification and Characterisation of HPC4-Tagged VWF Fragments

Some VWF fragments are cloned and expressed with a C-terminal HPC4 tag: EDQVDPRLIDGK (SEQ ID NO 38). Sometimes an additional linker with the sequence of ALA is introduced between the VWF fragment and the HPC4 tag. After cloning, expression and cell culturing the cell media is added CaCl₂ to a final concentration of 1 mM. The media is passed over an anti-HPC4 column. The column is equilibrated with 20 mM HEPES, 100 mM NaCl, 1 mM CaCl₂,

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pH=7.5. After application of the cell media, the column is washed with 20 mM HEPES, 1M NaCl, 1 mM CaCl₂, pH=7.5 and the HPC4-tagged VWF fragment is subsequently eluted with 20 mM HEPES, 100 mM NaCl, 5 mM EDTA, pH=7.5. The pool from the anti-HPC4 column is added 3 volumes of water to reduce the conductivity and applied onto a Mono Q column. Prior to the application the Mono Q column is equilibrated with 20 mM HEPES, 100 mM NaCl, 5 mM EDTA, pH=7.5. The Mono Q column is washed with 20 mM HEPES, 100 mM NaCl, pH=7.5 and the VWF fragment is eluted with a gradient from 100 mM NaCl to 2M NaCl in 20 mM HEPES, 10 mM CaCl₂, pH=7.5.

The purified protein is characterised by 1) SDS-gel electrophoreses, 2) analytical HPLC and 3) amino acid sequence analysis.

Example 40

Purification and Characterisation of Non HPC4-Tagged VWF Fragment

After cloning, expression and cell culturing the cell media is passed over an anti-VWF-Sepharose column. This column consists of an antibody against the N-terminal part of VWF coupled to Sepharose. The antibody is characterised by binding to the VWF fragment at neutral pH but not binding the VWF fragment at weak acid pH. This allow the VWF fragment to be bound when passing cell culture media over the column at neutral pH. Hereafter the column is washed with a buffer at neutral pH where after the VWF fragment is eluted from the column with a buffer at a weak acid pH (e.g. pH in the range from 3.0 to 6.5). The eluted VWF fragment is further purified by a combination classical purification steps such as ion-exchange chromatography, hydrophobic interaction chromatography and gel filtration.

The purified VWF fragment is characterised by 1) SDS-gel electrophoreses, 2) analytical HPLC and 3) amino acid sequence analysis.

Example 41

Bioavailability of a FVIII after Subcutaneous (s.c.) Administration Co-Formulated with VWF Fragment

A FVIII compound e.g. GlycoPEGylated FVIII, i.e. "N8-GP" (prepared essentially as disclosed in example 1+2 in WO2009108806) or another conjugated or non-conjugated FVIII at 2000 IU/ml or 1.2 µM is co-formulated with VWF fragment 764-1242 or 764-1482 at a concentration that enables the majority of FVIII to be bound to a VWF fragment compound in the injection composition. The binding of the VWF fragment to FVIII and the % saturation of the FVIII can be determined from the concentration of FVIII and VWF fragment in the composition and from experiments evaluating the binding affinity of the VWF fragment to the FVIII compound such as e.g. surface plasmon resonance experiments.

Test compounds are formulated in 18 mg/ml NaCl, 3 mg/ml saccharose, 1.5 mg/ml L-histidine, 0.1 mg/ml polysorbate 80, 0.25 mg/ml CaCl₂, pH 7.3. FVIII KO mice, exon 16 knock-out in a mixed background of C57Bl/6 and SV129, bred at Taconic M&B (B6.129S4-F8tm1Kaz/J) with an approximate weight of 22 g are dosed subcutaneously in the flank with 10000 U/kg FVIII or FVIII/VWF, 6 mice per test compound. Blood are sampled at 1, 3, 7, 17, 24, 30, 48, 72 and 96 h post administration. The mice are anaesthetized by isoflurane/O₂/N₂O prior to blood sampling via the retroorbital plexus. Three samples are taken from each mouse. Blood (45 µl) are stabilised with 5 µl of sodium-citrate (0.13 M) and added 200 µl FVIII Coatest SP buffer (50 mM TRIS-HCl, 1%

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BSA, Ciprofloxacin 10 mg/L, pH 7.3). After centrifugation at 4000 g for 5 minutes at room temperature are supernatants immediately frozen on dry ice before storage at -80° C. prior to analysis. FVIII activity is measured in a chromogenic assay as described by Øvlsen K et al. J. Thromb. Haemost, 2008, 6: 969-975 and FVIII antigen is analysed using two FVIII light chain antibodies (4F45 and 4F11) in a FVIII LOCI assay (Luminescence oxygen channelling immunoassay).

Mean plasma concentration versus time data are analysed by non-compartmental analysis using WinNonlin Phoenix (Pharsight Corporation) estimating the given pharmacokinetic parameters. The bioavailability is estimated by comparing the AUC/dose after s.c. administration with AUC/dose after i.v. administration of the FVIII compound in FVIII KO mice.

Example 42

Immunogenicity of VWF Fragments

The immunogenicity of VWF fragment 764-1242 or 764-1482 relative to other VWF fragments and full-length VWF is evaluated in a species capable of ADAM28-mediated cleavage of VWF, e.g. mice.

ADAM28 (A Disintegrin And Metalloproteinase Domain 28) has been described to cleave VWF (Mochizuki et al. J Natl Cancer Inst 2012; 104: 906-922) and is according to GeneCard® expressed on lymphocytes.

The relative immunogenicity is evaluated from the titer of VWF binding antibodies at certain time points after administration of VWF fragment 764-1242 or 764-1482 and comparator VWF fragments, e.g. VWF 764-1464 or full-length VWF. The assay for detection of VWF binding antibodies is a radioimmunoassay (RIA). Briefly, anti-VWF antibodies from a sample bind to radioactive ¹²⁵I-labelled VWF (full-length or fragments). Immunoglobulin and immune complexes bind to protein G-sepharose and is precipitated by centrifugation. The radioactivity in the precipitate is measured and this is proportional to the amount of anti-VWF antibodies in the sample. The result is expressed in percent of the total amount of added radioactivity, i.e. as % bound/total (% B/T).

The appearance of anti-VWF antibodies is evaluated after repeated (e.g. once weekly for 4 weeks or once daily for three weeks) s.c. or i.v. administration of the compounds in naïve mice, in VWF k/o mice as well as in mice tolerized to human VWF. Mice are injected weekly for e.g. eight weeks s.c. or i.v. with e.g. 1 µg VWF or the corresponding molar concentration (based on monomer content) of VWF fragments. The readout is the ratio of animals with positive titres at certain time points after the first and/or the last administration (e.g. 1, 2, 3, 4, 5, 6, 7 or 8 weeks). VWF k/o mice are injected weekly e.g. with VWF fragment or full-length VWF. For daily s.c. administration, the VWF dose is lower and based upon the bioavailability of the VWF fragment. Mice tolerized to hVWF are injected weekly for e.g. eight weeks s.c. with e.g. 1 µg VWF (or the corresponding molar concentration (based on monomer content) of VWF fragments). In some experiments the VWF is combined with complete Freund's adjuvant (CFA) for the first injection followed by weekly challenges by incomplete Freund's adjuvant (IFA).

Example 43

FVIII Degradation: Determination of FVIII Free Light Chain by Size-Exclusion Chromatography (SEC)

The dissociation of the rFVIII compound into free heavy and light chains is evaluated by a SEC method. The column is

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Sepax Zenix™ SEC-300 and the eluent is 10 mM Tris, 10 mM CaCl₂, 300 mM NaCl and 5% isopropanol, pH 7.0 Degradation of Factor VIII molecules is observed in SEC as appearance of a peak with longer elution times than monomeric Factor VIII. This peak has been assigned to free Light Chain (free LC).

Example 44

Stabilising Effect of vWF on Liquid FVIII Stability.

Formulations of Glycopegylated B-domain truncated/deleted FVIII ("GP-BDD-FVIII") with and without a vWF fragment were prepared. The vWF fragment was VWF(764-1464)—C1099/1142S (SEQ ID NO 19), with a C-terminal HPC4-tag added to facilitate purification. Both formulations contained about 0.85 μM GP-BDD-FVIII, 190 mM NaCl, 1.8 mM CaCl₂, 0.03 mg/ml polysorbate 80, 0.07 mg/ml Methionine, 10 mM sucrose, 12 mM Histidine and had a pH close to 6.9. One of the formulations furthermore contained 1.2 μM of a vWF fragment. The two samples were incubated for 4 weeks at 5° C. and assayed for free Light Chain by SEC chromatography. In order to test for the influence of the vWF

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on the chromatography of GP-BDD-FVIII, the samples without vWF fragment was split in two after the 4 weeks of incubation, and one of the resulting samples had vWF fragment added to a final concentration of 1.2 μM just prior to analysis. The amount of free Light Chain measured in the different samples is shown in the following table:

TABLE 17

GP-BDD-FVIII concentration	vWF fragment concentration during incubation	vWF fragment added just before SEC analysis	% free Light Chain after 4 weeks at 5° C.
0.85 μM	1.2 μM	—	1.1%
0.85 μM	—	—	5.1%
0.85 μM	—	1.2 μM	4.5%

It is seen that much less free Light Chain is observed after incubation with the vWF fragment. Addition of vWF just prior to analysis does not affect the result much, which shows that the effect is not a chromatographic artefact, but results from a stabilising action of the vWF fragment on GP-BDD-FVIII.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 58

<210> SEQ ID NO 1

<211> LENGTH: 2332

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1 5 10 15

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
20 25 30

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
35 40 45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
50 55 60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65 70 75 80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85 90 95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100 105 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205

-continued

His 210	Ser	Glu	Thr	Lys	Asn 215	Ser	Leu	Met	Gln	Asp	Arg 220	Asp	Ala	Ala	Ser
Ala 225	Arg	Ala	Trp	Pro	Lys 230	Met	His	Thr	Val	Asn 235	Gly	Tyr	Val	Asn	Arg 240
Ser	Leu	Pro	Gly	Leu 245	Ile	Gly	Cys	His	Arg 250	Lys	Ser	Val	Tyr	Trp	His 255
Val	Ile	Gly	Met	Gly 260	Thr	Thr	Pro	Glu	Val 265	His	Ser	Ile	Phe	Leu	Glu
Gly	His	Thr 275	Phe	Leu	Val	Arg	Asn 280	His	Arg	Gln	Ala	Ser 285	Leu	Glu	Ile
Ser 290	Pro	Ile	Thr	Phe	Leu	Thr 295	Ala	Gln	Thr	Leu	Leu 300	Met	Asp	Leu	Gly
Gln 305	Phe	Leu	Leu	Phe	Cys 310	His	Ile	Ser	Ser	His 315	Gln	His	Asp	Gly	Met 320
Glu	Ala	Tyr	Val	Lys 325	Val	Asp	Ser	Cys	Pro 330	Glu	Glu	Pro	Gln	Leu	Arg 335
Met	Lys	Asn 340	Asn	Glu	Glu	Ala	Glu	Asp 345	Tyr	Asp	Asp	Asp	Leu	Thr	Asp 350
Ser	Glu	Met 355	Asp	Val	Val	Arg	Phe 360	Asp	Asp	Asp	Asn 365	Ser	Pro	Ser	Phe
Ile 370	Gln	Ile	Arg	Ser	Val	Ala 375	Lys	Lys	His	Pro	Lys 380	Thr	Trp	Val	His
Tyr 385	Ile	Ala	Ala	Glu	Glu 390	Glu	Asp	Trp	Asp	Tyr 395	Ala	Pro	Leu	Val	Leu 400
Ala	Pro	Asp	Asp	Arg 405	Ser	Tyr	Lys	Ser	Gln 410	Tyr	Leu	Asn	Asn	Gly	Pro 415
Gln	Arg	Ile	Gly	Arg 420	Lys	Tyr	Lys	Lys	Val 425	Arg	Phe	Met	Ala	Tyr	Thr 430
Asp	Glu	Thr 435	Phe	Lys	Thr	Arg	Glu	Ala 440	Ile	Gln	His	Glu 445	Ser	Gly	Ile
Leu	Gly 450	Pro	Leu	Leu	Tyr	Gly 455	Glu	Val	Gly	Asp 460	Thr	Leu	Leu	Ile	Ile
Phe 465	Lys	Asn	Gln	Ala	Ser 470	Arg	Pro	Tyr	Asn	Ile 475	Tyr	Pro	His	Gly	Ile 480
Thr	Asp	Val	Arg	Pro 485	Leu	Tyr	Ser	Arg	Arg 490	Leu	Pro	Lys	Gly	Val	Lys 495
His	Leu	Lys 500	Asp	Phe	Pro	Ile	Leu	Pro 505	Gly	Glu	Ile	Phe	Lys	Tyr	Lys 510
Trp	Thr	Val 515	Thr	Val	Glu	Asp	Gly 520	Pro	Thr	Lys	Ser	Asp 525	Pro	Arg	Cys
Leu 530	Thr	Arg	Tyr	Tyr	Ser 535	Ser	Phe	Val	Asn	Met	Glu 540	Arg	Asp	Leu	Ala
Ser 545	Gly	Leu	Ile	Gly	Pro 550	Leu	Leu	Ile	Cys	Tyr 555	Lys	Glu	Ser	Val	Asp 560
Gln	Arg	Gly	Asn	Gln 565	Ile	Met	Ser	Asp	Lys 570	Arg	Asn	Val	Ile	Leu	Phe 575
Ser	Val	Phe 580	Asp	Glu	Asn	Arg	Ser	Trp 585	Tyr	Leu	Thr	Glu	Asn	Ile	Gln 590
Arg	Phe	Leu 595	Pro	Asn	Pro	Ala	Gly	Val 600	Gln	Leu	Glu	Asp	Pro	Glu	Phe 605
Gln 610	Ala	Ser	Asn	Ile	Met	His 615	Ser	Ile	Asn	Gly	Tyr	Val	Phe	Asp	Ser 620

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Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	Tyr	Ile	Leu	625	630	635	640
Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	Ser	Gly	Tyr	645	650	655	
Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	Leu	Phe	Pro	660	665	670	
Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	Gly	Leu	Trp	675	680	685	
Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	Met	Thr	Ala	690	695	700	
Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	Tyr	Tyr	Glu	705	710	715	720
Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	Asn	Asn	Ala	725	730	735	
Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Ser	Arg	His	Pro	Ser	Thr	Arg	740	745	750	
Gln	Lys	Gln	Phe	Asn	Ala	Thr	Thr	Ile	Pro	Glu	Asn	Asp	Ile	Glu	Lys	755	760	765	
Thr	Asp	Pro	Trp	Phe	Ala	His	Arg	Thr	Pro	Met	Pro	Lys	Ile	Gln	Asn	770	775	780	
Val	Ser	Ser	Ser	Asp	Leu	Leu	Met	Leu	Leu	Arg	Gln	Ser	Pro	Thr	Pro	785	790	795	800
His	Gly	Leu	Ser	Leu	Ser	Asp	Leu	Gln	Glu	Ala	Lys	Tyr	Glu	Thr	Phe	805	810	815	
Ser	Asp	Asp	Pro	Ser	Pro	Gly	Ala	Ile	Asp	Ser	Asn	Asn	Ser	Leu	Ser	820	825	830	
Glu	Met	Thr	His	Phe	Arg	Pro	Gln	Leu	His	His	Ser	Gly	Asp	Met	Val	835	840	845	
Phe	Thr	Pro	Glu	Ser	Gly	Leu	Gln	Leu	Arg	Leu	Asn	Glu	Lys	Leu	Gly	850	855	860	
Thr	Thr	Ala	Ala	Thr	Glu	Leu	Lys	Lys	Leu	Asp	Phe	Lys	Val	Ser	Ser	865	870	875	880
Thr	Ser	Asn	Asn	Leu	Ile	Ser	Thr	Ile	Pro	Ser	Asp	Asn	Leu	Ala	Ala	885	890	895	
Gly	Thr	Asp	Asn	Thr	Ser	Ser	Leu	Gly	Pro	Pro	Ser	Met	Pro	Val	His	900	905	910	
Tyr	Asp	Ser	Gln	Leu	Asp	Thr	Thr	Leu	Phe	Gly	Lys	Lys	Ser	Ser	Pro	915	920	925	
Leu	Thr	Glu	Ser	Gly	Gly	Pro	Leu	Ser	Leu	Ser	Glu	Glu	Asn	Asn	Asp	930	935	940	
Ser	Lys	Leu	Leu	Glu	Ser	Gly	Leu	Met	Asn	Ser	Gln	Glu	Ser	Ser	Trp	945	950	955	960
Gly	Lys	Asn	Val	Ser	Ser	Thr	Glu	Ser	Gly	Arg	Leu	Phe	Lys	Gly	Lys	965	970	975	
Arg	Ala	His	Gly	Pro	Ala	Leu	Leu	Thr	Lys	Asp	Asn	Ala	Leu	Phe	Lys	980	985	990	
Val	Ser	Ile	Ser	Leu	Leu	Lys	Thr	Asn	Lys	Thr	Ser	Asn	Asn	Ser	Ala	995	1000	1005	
Thr	Asn	Arg	Lys	Thr	His	Ile	Asp	Gly	Pro	Ser	Leu	Leu	Ile	Glu		1010	1015	1020	
Asn	Ser	Pro	Ser	Val	Trp	Gln	Asn	Ile	Leu	Glu	Ser	Asp	Thr	Glu		1025	1030	1035	
Phe	Lys	Lys	Val	Thr	Pro	Leu	Ile	His	Asp	Arg	Met	Leu	Met	Asp					

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1040	1045	1050
Lys Asn Ala Thr Ala Leu Arg	Leu Asn His Met Ser	Asn Lys Thr
1055	1060	1065
Thr Ser Ser Lys Asn Met Glu	Met Val Gln Gln Lys	Lys Glu Gly
1070	1075	1080
Pro Ile Pro Pro Asp Ala Gln	Asn Pro Asp Met Ser	Phe Phe Lys
1085	1090	1095
Met Leu Phe Leu Pro Glu Ser	Ala Arg Trp Ile Gln	Arg Thr His
1100	1105	1110
Gly Lys Asn Ser Leu Asn Ser	Gly Gln Gly Pro Ser	Pro Lys Gln
1115	1120	1125
Leu Val Ser Leu Gly Pro Glu	Lys Ser Val Glu Gly	Gln Asn Phe
1130	1135	1140
Leu Ser Glu Lys Asn Lys Val	Val Val Gly Lys Gly	Glu Phe Thr
1145	1150	1155
Lys Asp Val Gly Leu Lys Glu	Met Val Phe Pro Ser	Ser Arg Asn
1160	1165	1170
Leu Phe Leu Thr Asn Leu Asp	Asn Leu His Glu Asn	Asn Thr His
1175	1180	1185
Asn Gln Glu Lys Lys Ile Gln	Glu Glu Ile Glu Lys	Lys Glu Thr
1190	1195	1200
Leu Ile Gln Glu Asn Val Val	Leu Pro Gln Ile His	Thr Val Thr
1205	1210	1215
Gly Thr Lys Asn Phe Met Lys	Asn Leu Phe Leu Leu	Ser Thr Arg
1220	1225	1230
Gln Asn Val Glu Gly Ser Tyr	Asp Gly Ala Tyr Ala	Pro Val Leu
1235	1240	1245
Gln Asp Phe Arg Ser Leu Asn	Asp Ser Thr Asn Arg	Thr Lys Lys
1250	1255	1260
His Thr Ala His Phe Ser Lys	Lys Gly Glu Glu Glu	Asn Leu Glu
1265	1270	1275
Gly Leu Gly Asn Gln Thr Lys	Gln Ile Val Glu Lys	Tyr Ala Cys
1280	1285	1290
Thr Thr Arg Ile Ser Pro Asn	Thr Ser Gln Gln Asn	Phe Val Thr
1295	1300	1305
Gln Arg Ser Lys Arg Ala Leu	Lys Gln Phe Arg Leu	Pro Leu Glu
1310	1315	1320
Glu Thr Glu Leu Glu Lys Arg	Ile Ile Val Asp Asp	Thr Ser Thr
1325	1330	1335
Gln Trp Ser Lys Asn Met Lys	His Leu Thr Pro Ser	Thr Leu Thr
1340	1345	1350
Gln Ile Asp Tyr Asn Glu Lys	Glu Lys Gly Ala Ile	Thr Gln Ser
1355	1360	1365
Pro Leu Ser Asp Cys Leu Thr	Arg Ser His Ser Ile	Pro Gln Ala
1370	1375	1380
Asn Arg Ser Pro Leu Pro Ile	Ala Lys Val Ser Ser	Phe Pro Ser
1385	1390	1395
Ile Arg Pro Ile Tyr Leu Thr	Arg Val Leu Phe Gln	Asp Asn Ser
1400	1405	1410
Ser His Leu Pro Ala Ala Ser	Tyr Arg Lys Lys Asp	Ser Gly Val
1415	1420	1425
Gln Glu Ser Ser His Phe Leu	Gln Gly Ala Lys Lys	Asn Asn Leu
1430	1435	1440

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Ser Leu	Ala Ile	Leu Thr	Leu	Glu Met	Thr Gly	Asp	Gln Arg	Glu	
1445			1450			1455			
Val Gly	Ser Leu	Gly Thr	Ser	Ala Thr	Asn Ser	Val	Thr Tyr	Lys	
1460			1465			1470			
Lys Val	Glu Asn	Thr Val	Leu	Pro Lys	Pro Asp	Leu	Pro Lys	Thr	
1475			1480			1485			
Ser Gly	Lys Val	Glu Leu	Leu	Pro Lys	Val His	Ile	Tyr Gln	Lys	
1490			1495			1500			
Asp Leu	Phe Pro	Thr Glu	Thr	Ser Asn	Gly Ser	Pro	Gly His	Leu	
1505			1510			1515			
Asp Leu	Val Glu	Gly Ser	Leu	Leu Gln	Gly Thr	Glu	Gly Ala	Ile	
1520			1525			1530			
Lys Trp	Asn Glu	Ala Asn	Arg	Pro Gly	Lys Val	Pro	Phe Leu	Arg	
1535			1540			1545			
Val Ala	Thr Glu	Ser Ser	Ala	Lys Thr	Pro Ser	Lys	Leu Leu	Asp	
1550			1555			1560			
Pro Leu	Ala Trp	Asp Asn	His	Tyr Gly	Thr Gln	Ile	Pro Lys	Glu	
1565			1570			1575			
Glu Trp	Lys Ser	Gln Glu	Lys	Ser Pro	Glu Lys	Thr	Ala Phe	Lys	
1580			1585			1590			
Lys Lys	Asp Thr	Ile Leu	Ser	Leu Asn	Ala Cys	Glu	Ser Asn	His	
1595			1600			1605			
Ala Ile	Ala Ala	Ile Asn	Glu	Gly Gln	Asn Lys	Pro	Glu Ile	Glu	
1610			1615			1620			
Val Thr	Trp Ala	Lys Gln	Gly	Arg Thr	Glu Arg	Leu	Cys Ser	Gln	
1625			1630			1635			
Asn Pro	Pro Val	Leu Lys	Arg	His Gln	Arg Glu	Ile	Thr Arg	Thr	
1640			1645			1650			
Thr Leu	Gln Ser	Asp Gln	Glu	Glu Ile	Asp Tyr	Asp	Asp Thr	Ile	
1655			1660			1665			
Ser Val	Glu Met	Lys Lys	Glu	Asp Phe	Asp Ile	Tyr	Asp Glu	Asp	
1670			1675			1680			
Glu Asn	Gln Ser	Pro Arg	Ser	Phe Gln	Lys Lys	Thr	Arg His	Tyr	
1685			1690			1695			
Phe Ile	Ala Ala	Val Glu	Arg	Leu Trp	Asp Tyr	Gly	Met Ser	Ser	
1700			1705			1710			
Ser Pro	His Val	Leu Arg	Asn	Arg Ala	Gln Ser	Gly	Ser Val	Pro	
1715			1720			1725			
Gln Phe	Lys Lys	Val Val	Phe	Gln Glu	Phe Thr	Asp	Gly Ser	Phe	
1730			1735			1740			
Thr Gln	Pro Leu	Tyr Arg	Gly	Glu Leu	Asn Glu	His	Leu Gly	Leu	
1745			1750			1755			
Leu Gly	Pro Tyr	Ile Arg	Ala	Glu Val	Glu Asp	Asn	Ile Met	Val	
1760			1765			1770			
Thr Phe	Arg Asn	Gln Ala	Ser	Arg Pro	Tyr Ser	Phe	Tyr Ser	Ser	
1775			1780			1785			
Leu Ile	Ser Tyr	Glu Glu	Asp	Gln Arg	Gln Gly	Ala	Glu Pro	Arg	
1790			1795			1800			
Lys Asn	Phe Val	Lys Pro	Asn	Glu Thr	Lys Thr	Tyr	Phe Trp	Lys	
1805			1810			1815			
Val Gln	His His	Met Ala	Pro	Thr Lys	Asp Glu	Phe	Asp Cys	Lys	
1820			1825			1830			

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Ala Trp 1835	Ala Tyr Phe Ser Asp 1840	Val Asp Leu Glu Lys 1845	Asp Val His
Ser Gly 1850	Leu Ile Gly Pro Leu 1855	Leu Val Cys His Thr 1860	Asn Thr Leu
Asn Pro 1865	Ala His Gly Arg Gln 1870	Val Thr Val Gln Glu 1875	Phe Ala Leu
Phe Phe 1880	Thr Ile Phe Asp Glu 1885	Thr Lys Ser Trp Tyr 1890	Phe Thr Glu
Asn Met 1895	Glu Arg Asn Cys Arg 1900	Ala Pro Cys Asn Ile 1905	Gln Met Glu
Asp Pro 1910	Thr Phe Lys Glu Asn 1915	Tyr Arg Phe His Ala 1920	Ile Asn Gly
Tyr Ile 1925	Met Asp Thr Leu Pro 1930	Gly Leu Val Met Ala 1935	Gln Asp Gln
Arg Ile 1940	Arg Trp Tyr Leu Leu 1945	Ser Met Gly Ser Asn 1950	Glu Asn Ile
His Ser 1955	Ile His Phe Ser Gly 1960	His Val Phe Thr Val 1965	Arg Lys Lys
Glu Glu 1970	Tyr Lys Met Ala Leu 1975	Tyr Asn Leu Tyr Pro 1980	Gly Val Phe
Glu Thr 1985	Val Glu Met Leu Pro 1990	Ser Lys Ala Gly Ile 1995	Trp Arg Val
Glu Cys 2000	Leu Ile Gly Glu His 2005	Leu His Ala Gly Met 2010	Ser Thr Leu
Phe Leu 2015	Val Tyr Ser Asn Lys 2020	Cys Gln Thr Pro Leu 2025	Gly Met Ala
Ser Gly 2030	His Ile Arg Asp Phe 2035	Gln Ile Thr Ala Ser 2040	Gly Gln Tyr
Gly Gln 2045	Trp Ala Pro Lys Leu 2050	Ala Arg Leu His Tyr 2055	Ser Gly Ser
Ile Asn 2060	Ala Trp Ser Thr Lys 2065	Glu Pro Phe Ser Trp 2070	Ile Lys Val
Asp Leu 2075	Leu Ala Pro Met Ile 2080	Ile His Gly Ile Lys 2085	Thr Gln Gly
Ala Arg 2090	Gln Lys Phe Ser Ser 2095	Leu Tyr Ile Ser Gln 2100	Phe Ile Ile
Met Tyr 2105	Ser Leu Asp Gly Lys 2110	Lys Trp Gln Thr Tyr 2115	Arg Gly Asn
Ser Thr 2120	Gly Thr Leu Met Val 2125	Phe Phe Gly Asn Val 2130	Asp Ser Ser
Gly Ile 2135	Lys His Asn Ile Phe 2140	Asn Pro Pro Ile Ile 2145	Ala Arg Tyr
Ile Arg 2150	Leu His Pro Thr His 2155	Tyr Ser Ile Arg Ser 2160	Thr Leu Arg
Met Glu 2165	Leu Met Gly Cys Asp 2170	Leu Asn Ser Cys Ser 2175	Met Pro Leu
Gly Met 2180	Glu Ser Lys Ala Ile 2185	Ser Asp Ala Gln Ile 2190	Thr Ala Ser
Ser Tyr 2195	Phe Thr Asn Met Phe 2200	Ala Thr Trp Ser Pro 2205	Ser Lys Ala
Arg Leu 2210	His Leu Gln Gly Arg 2215	Ser Asn Ala Trp Arg 2220	Pro Gln Val
Asn Asn	Pro Lys Glu Trp Leu	Gln Val Asp Phe Gln	Lys Thr Met

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2225                2230                2235
Lys Val  Thr Gly Val Thr Thr  Gln Gly Val Lys Ser  Leu Leu Thr
2240                2245                2250

Ser Met  Tyr Val Lys Glu Phe  Leu Ile Ser Ser Ser  Gln Asp Gly
2255                2260                2265

His Gln  Trp Thr Leu Phe Phe  Gln Asn Gly Lys Val  Lys Val Phe
2270                2275                2280

Gln Gly  Asn Gln Asp Ser Phe  Thr Pro Val Val Asn  Ser Leu Asp
2285                2290                2295

Pro Pro  Leu Leu Thr Arg Tyr  Leu Arg Ile His Pro  Gln Ser Trp
2300                2305                2310

Val His  Gln Ile Ala Leu Arg  Met Glu Val Leu Gly  Cys Glu Ala
2315                2320                2325

Gln Asp  Leu Tyr
2330

<210> SEQ ID NO 2
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Linker sequence

<400> SEQUENCE: 2

Ser Phe Ser Gln Asn Ser Arg His Pro Ser Gln Asn Pro Pro Val Leu
1          5          10          15

Lys Arg His Gln Arg
20

<210> SEQ ID NO 3
<211> LENGTH: 1667
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 226 amino acid B domain FVIII variant

<400> SEQUENCE: 3

Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1          5          10          15

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
20          25          30

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
35          40          45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
50          55          60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65          70          75          80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85          90          95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100         105         110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115         120         125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130         135         140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145         150         155         160

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His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	Gly	Ala	Leu
			165						170					175	
Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	Gln	Thr	Leu
			180					185					190		
His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly	Lys	Ser	Trp
			195				200					205			
His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp	Ala	Ala	Ser
			210			215				220					
Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr	Val	Asn	Arg
225					230					235					240
Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val	Tyr	Trp	His
			245						250					255	
Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile	Phe	Leu	Glu
			260					265					270		
Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser	Leu	Glu	Ile
			275				280					285			
Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met	Asp	Leu	Gly
			290			295				300					
Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His	Asp	Gly	Met
305					310					315					320
Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro	Gln	Leu	Arg
			325						330					335	
Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp	Leu	Thr	Asp
			340					345					350		
Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser	Pro	Ser	Phe
			355				360					365			
Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	His	Pro	Lys	Thr	Trp	Val	His
			370			375				380					
Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro	Leu	Val	Leu
385					390					395					400
Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn	Asn	Gly	Pro
			405						410				415		
Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met	Ala	Tyr	Thr
			420					425					430		
Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu	Ser	Gly	Ile
			435				440					445			
Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu	Leu	Ile	Ile
			450			455				460					
Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro	His	Gly	Ile
465					470					475					480
Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys	Gly	Val	Lys
			485						490				495		
His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe	Lys	Tyr	Lys
			500					505				510			
Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	Pro	Arg	Cys
			515				520					525			
Leu	Thr	Arg	T												

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580						585						590					
Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp	Pro	Glu	Phe		
		595					600					605					
Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	Phe	Asp	Ser		
	610					615					620						
Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	Tyr	Ile	Leu		
	625				630					635					640		
Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	Ser	Gly	Tyr		
				645					650					655			
Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	Leu	Phe	Pro		
				660					665					670			
Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	Gly	Leu	Trp		
		675					680					685					
Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	Met	Thr	Ala		
	690					695					700						
Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	Tyr	Tyr	Glu		
	705				710					715					720		
Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	Asn	Asn	Ala		
				725					730					735			
Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Ser	Arg	His	Pro	Ser	Thr	Arg		
			740					745						750			
Gln	Lys	Gln	Phe	Asn	Ala	Thr	Thr	Ile	Pro	Glu	Asn	Asp	Ile	Glu	Lys		
		755						760					765				
Thr	Asp	Pro	Trp	Phe	Ala	His	Arg	Thr	Pro	Met	Pro	Lys	Ile	Gln	Asn		
	770					775					780						
Val	Ser	Ser	Ser	Asp	Leu	Leu	Met	Leu	Leu	Arg	Gln	Ser	Pro	Thr	Pro		
	785				790					795					800		
His	Gly	Leu	Ser	Leu	Ser	Asp	Leu	Gln	Glu	Ala	Lys	Tyr	Glu	Thr	Phe		
				805					810					815			
Ser	Asp	Asp	Pro	Ser	Pro	Gly	Ala	Ile	Asp	Ser	Asn	Asn	Ser	Leu	Ser		
			820					825						830			
Glu	Met	Thr	His	Phe	Arg	Pro	Gln	Leu	His	His	Ser	Gly	Asp	Met	Val		
		835					840						845				
Phe	Thr	Pro	Glu	Ser	Gly	Leu	Gln	Leu	Arg	Leu	Asn	Glu	Lys	Leu	Gly		
	850					855					860						
Thr	Thr	Ala	Ala	Thr	Glu	Leu	Lys	Lys	Leu	Asp	Phe	Lys	Val	Ser	Ser		
	865				870					875					880		
Thr	Ser	Asn	Asn	Leu	Ile	Ser	Thr	Ile	Pro	Ser	Asp	Asn	Leu	Ala	Ala		
				885					890					895			
Gly	Thr	Asp	Asn	Thr	Ser	Ser	Leu	Gly	Pro	Pro	Ser	Met	Pro	Val	His		
			900					905						910			
Tyr	Asp	Ser	Gln	Leu	Asp	Thr	Thr	Leu	Phe	Gly	Lys	Lys	Ser	Ser	Pro		
	915						920						925				
Leu	Thr	Glu	Ser	Gly	Gly	Pro	Leu	Ser	Leu	Ser	Glu	Glu	Asn	Asn	Asp		
	930					935						940					
Ser	Lys	Leu	Leu	Glu	Ser	Gly	Leu	Met	Asn	Ser	Gln	Glu	Ser	Ser	Trp		
	945				950					955					960		
Gly	Lys	Asn	Val	Ser	His	His	His	His	His	His	Ser	Gln	Asn	Pro	Pro		
				965					970					975			
Val	Leu	Lys	Arg	His	Gln	Arg	Glu	Ile	Thr	Arg	Thr	Thr	Leu	Gln	Ser		
			980					985						990			
Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu	Met	Lys		
		995					1000						1005				

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Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser	Pro
1010						1015					1020			
Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val
1025						1030					1035			
Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu
1040						1045					1050			
Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val
1055						1060					1065			
Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr
1070						1075					1080			
Arg	Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile
1085						1090					1095			
Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln
1100						1105					1110			
Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu
1115						1120					1125			
Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys
1130						1135					1140			
Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met
1145						1150					1155			
Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe
1160						1165					1170			
Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His	Ser	Gly	Leu	Ile	Gly
1175						1180					1185			
Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	Gly
1190						1195					1200			
Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe
1205						1210					1215			
Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn
1220						1225					1230			
Cys	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe	Lys
1235						1240					1245			
Glu	Asn	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	Thr
1250						1255					1260			
Leu	Pro	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg	Trp	Tyr
1265						1270					1275			
Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His	Phe
1280						1285					1290			
Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met
1295						1300					1305			
Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met
1310						1315					1320			
Leu	Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly
1325						1330					1335			
Glu	His	Leu	His	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser
1340						1345					1350			
Asn	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg
1355						1360					1365			
Asp	Phe	Gln	Ile	Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro
1370						1375					1380			
Lys	Leu	Ala	Arg	Leu	His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser
1385						1390					1395			

Thr	Lys	Glu	Pro	Phe	Ser	Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	
1400						1405					1410				
Met	Ile	Ile	His	Gly	Ile	Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	
1415						1420					1425				
Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp	
1430						1435					1440				
Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	
1445						1450					1455				
Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	
1460						1465					1470				
Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	
1475						1480					1485				
Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	
1490						1495					1500				
Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	
1505						1510					1515				
Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn	
1520						1525					1530				
Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln	
1535						1540					1545				
Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys	Glu	
1550						1555					1560				
Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val	Thr	Gly	Val	
1565						1570					1575				
Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val	Lys	
1580						1585					1590				
Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly	His	Gln	Trp	Thr	Leu	
1595						1600					1605				
Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val	Phe	Gln	Gly	Asn	Gln	Asp	
1610						1615					1620				
Ser	Phe	Thr	Pro	Val	Val	Asn	Ser	Leu	Asp	Pro	Pro	Leu	Leu	Thr	
1625						1630					1635				
Arg	Tyr	Leu	Arg	Ile	His	Pro	Gln	Ser	Trp	Val	His	Gln	Ile	Ala	
1640						1645					1650				
Leu	Arg	Met	Glu	Val	Leu	Gly	Cys	Glu	Ala	Gln	Asp	Leu	Tyr		
1655						1660					1665				
<210> SEQ ID NO 4															
<211> LENGTH: 65															
<212> TYPE: PRT															
<213> ORGANISM: Artificial Sequence															
<220> FEATURE:															
<223> OTHER INFORMATION: vWF fragment: amino acids 764-828 (TIL')															
<400> SEQUENCE: 4															
Ser	Leu	Ser	Cys	Arg	Pro	Pro	Met	Val	Lys	Leu	Val	Cys	Pro	Ala	Asp
1				5					10					15	
Asn	Leu	Arg	Ala	Glu	Gly	Leu	Glu	Cys	Thr	Lys	Thr	Cys	Gln	Asn	Tyr
			20					25					30		
Asp	Leu	Glu	Cys	Met	Ser	Met	Gly	Cys	Val	Ser	Gly	Cys	Leu	Cys	Pro
			35				40					45			
Pro	Gly	Met	Val	Arg	His	Glu	Asn	Arg	Cys	Val	Ala	Leu	Glu	Arg	Cys
						55					60				
Pro															

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<210> SEQ ID NO 5
 <211> LENGTH: 102
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: vWF fragment: amino acids 764-865 (TIL'/E')

<400> SEQUENCE: 5

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
 1 5 10 15
 Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
 20 25 30
 Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
 35 40 45
 Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
 50 55 60
 Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
 65 70 75 80
 Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
 85 90 95
 Asp His Val Cys Asp Ala
 100

<210> SEQ ID NO 6
 <211> LENGTH: 272
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: vWF fragment: amino acids 764-1035
 (TIL'/E'/VWD3 I)

<400> SEQUENCE: 6

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
 1 5 10 15
 Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
 20 25 30
 Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
 35 40 45
 Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
 50 55 60
 Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
 65 70 75 80
 Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
 85 90 95
 Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
 100 105 110
 Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
 115 120 125
 Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
 130 135 140
 Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
 145 150 155 160
 Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
 165 170 175
 Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
 180 185 190
 Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser

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195	200	205
Val Val Trp Asp Arg His	Leu Ser Ile Ser Val	Val Leu Lys Gln Thr
210	215	220
Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln		
225	230	235 240
Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val		
245	250	255
Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg		
260	265	270
<210> SEQ ID NO 7		
<211> LENGTH: 278		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: vWF fragment: amino acids 764-1041		
(TIL'/E'/VWD3 II)		
<400> SEQUENCE: 7		
Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp		
1	5	10 15
Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr		
20	25	30
Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro		
35	40	45
Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys		
50	55	60
Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys		
65	70	75 80
Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr		
85	90	95
Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr		
100	105	110
Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr		
115	120	125
Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile		
130	135	140
Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys		
145	150	155 160
Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly		
165	170	175
Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val		
180	185	190
Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser		
195	200	205
Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr		
210	215	220
Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln		
225	230	235 240
Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val		
245	250	255
Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg		
260	265	270
Lys Val Pro Leu Asp Ser		
275		

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<210> SEQ ID NO 8
<211> LENGTH: 282
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: vWF fragment: amino acids 764-1045
      (TIL'/E'/VWD3 III)

<400> SEQUENCE: 8

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
1          5          10          15

Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
20         25         30

Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
35         40         45

Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
50         55         60

Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
65         70         75         80

Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
85         90         95

Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
100        105        110

Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
115        120        125

Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
130        135        140

Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
145        150        155        160

Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
165        170        175

Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
180        185        190

Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser
195        200        205

Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr
210        215        220

Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln
225        230        235        240

Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val
245        250        255

Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg
260        265        270

Lys Val Pro Leu Asp Ser Ser Pro Ala Thr
275        280

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<210> SEQ ID NO 9
<211> LENGTH: 365
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: vWF fragment: amino acids 764-1128
      (TIL'/E'/VWD3/C8-3)

<400> SEQUENCE: 9

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Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
1          5          10          15

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Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
   20                               25           30

Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
   35                               40           45

Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
   50                               55           60

Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
   65                               70           75           80

Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
   85                               90           95

Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
  100                               105          110

Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
  115                               120          125

Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
  130                               135          140

Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
  145                               150          155          160

Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
  165                               170          175

Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
  180                               185          190

Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser
  195                               200          205

Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr
  210                               215          220

Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln
  225                               230          235          240

Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val
  245                               250          255

Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg
  260                               265          270

Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met
  275                               280          285

Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val
  290                               295          300

Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val
  305                               310          315          320

Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys
  325                               330          335

Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln His Gly
  340                               345          350

Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln
  355                               360          365

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<210> SEQ ID NO 10

<211> LENGTH: 435

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: vWF fragment: amino acids 764-1198

(TIL'/E'/VWD3/C8-3/TIL-3)

<400> SEQUENCE: 10

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Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
 1           5           10           15

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Asn	Leu	Arg	Ala	Glu	Gly	Leu	Glu	Cys	Thr	Lys	Thr	Cys	Gln	Asn	Tyr	
			20				25						30			
Asp	Leu	Glu	Cys	Met	Ser	Met	Gly	Cys	Val	Ser	Gly	Cys	Leu	Cys	Pro	
			35				40				45					
Pro	Gly	Met	Val	Arg	His	Glu	Asn	Arg	Cys	Val	Ala	Leu	Glu	Arg	Cys	
			50				55				60					
Pro	Cys	Phe	His	Gln	Gly	Lys	Glu	Tyr	Ala	Pro	Gly	Glu	Thr	Val	Lys	
65				70						75			80			
Ile	Gly	Cys	Asn	Thr	Cys	Val	Cys	Gln	Asp	Arg	Lys	Trp	Asn	Cys	Thr	
			85						90			95				
Asp	His	Val	Cys	Asp	Ala	Thr	Cys	Ser	Thr	Ile	Gly	Met	Ala	His	Tyr	
			100			105						110				
Leu	Thr	Phe	Asp	Gly	Leu	Lys	Tyr	Leu	Phe	Pro	Gly	Glu	Cys	Gln	Tyr	
			115			120						125				
Val	Leu	Val	Gln	Asp	Tyr	Cys	Gly	Ser	Asn	Pro	Gly	Thr	Phe	Arg	Ile	
			130			135						140				
Leu	Val	Gly	Asn	Lys	Gly	Cys	Ser	His	Pro	Ser	Val	Lys	Cys	Lys	Lys	
145				150						155			160			
Arg	Val	Thr	Ile	Leu	Val	Glu	Gly	Gly	Glu	Ile	Glu	Leu	Phe	Asp	Gly	
			165						170			175				
Glu	Val	Asn	Val	Lys	Arg	Pro	Met	Lys	Asp	Glu	Thr	His	Phe	Glu	Val	
			180			185						190				
Val	Glu	Ser	Gly	Arg	Tyr	Ile	Ile	Leu	Leu	Leu	Gly	Lys	Ala	Leu	Ser	
			195			200						205				
Val	Val	Trp	Asp	Arg	His	Leu	Ser	Ile	Ser	Val	Val	Leu	Lys	Gln	Thr	
			210			215						220				
Tyr	Gln	Glu	Lys	Val	Cys	Gly	Leu	Cys	Gly	Asn	Phe	Asp	Gly	Ile	Gln	
225				230						235			240			
Asn	Asn	Asp	Leu	Thr	Ser	Ser	Asn	Leu	Gln	Val	Glu	Glu	Asp	Pro	Val	
			245						250			255				
Asp	Phe	Gly	Asn	Ser	Trp	Lys	Val	Ser	Ser	Gln	Cys	Ala	Asp	Thr	Arg	
			260			265						270				
Lys	Val	Pro	Leu	Asp	Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met	
			275			280						285				
Lys	Gln	Thr	Met	Val	Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val	
			290			295						300				
Phe	Gln	Asp	Cys	Asn	Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val	
305				310						315			320			
Cys	Ile	Tyr	Asp	Thr	Cys	Ser	Cys	Glu	Ser	Ile	Gly	Asp	Cys	Ala	Cys	
			325						330			335				
Phe	Cys	Asp	Thr	Ile	Ala	Ala	Tyr	Ala	His	Val	Cys	Ala	Gln	His	Gly	
			340			345						350				
Lys	Val	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu	
			355			360						365				
Glu	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn	
			370			375						380				
Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu	
385				390						395			400			
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro	
			405						410			415				
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp	
			420			425						430				

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Cys Pro Val
435

<210> SEQ ID NO 11
 <211> LENGTH: 487
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: vWF fragment: amino acids 764-1250
 (TIL'/E'/D3 I

<400> SEQUENCE: 11

Ser	Leu	Ser	Cys	Arg	Pro	Pro	Met	Val	Lys	Leu	Val	Cys	Pro	Ala	Asp
1				5					10					15	
Asn	Leu	Arg	Ala	Glu	Gly	Leu	Glu	Cys	Thr	Lys	Thr	Cys	Gln	Asn	Tyr
			20					25					30		
Asp	Leu	Glu	Cys	Met	Ser	Met	Gly	Cys	Val	Ser	Gly	Cys	Leu	Cys	Pro
			35				40					45			
Pro	Gly	Met	Val	Arg	His	Glu	Asn	Arg	Cys	Val	Ala	Leu	Glu	Arg	Cys
			50			55					60				
Pro	Cys	Phe	His	Gln	Gly	Lys	Glu	Tyr	Ala	Pro	Gly	Glu	Thr	Val	Lys
65				70					75					80	
Ile	Gly	Cys	Asn	Thr	Cys	Val	Cys	Gln	Asp	Arg	Lys	Trp	Asn	Cys	Thr
			85						90					95	
Asp	His	Val	Cys	Asp	Ala	Thr	Cys	Ser	Thr	Ile	Gly	Met	Ala	His	Tyr
			100					105					110		
Leu	Thr	Phe	Asp	Gly	Leu	Lys	Tyr	Leu	Phe	Pro	Gly	Glu	Cys	Gln	Tyr
			115				120					125			
Val	Leu	Val	Gln	Asp	Tyr	Cys	Gly	Ser	Asn	Pro	Gly	Thr	Phe	Arg	Ile
			130			135					140				
Leu	Val	Gly	Asn	Lys	Gly	Cys	Ser	His	Pro	Ser	Val	Lys	Cys	Lys	Lys
145				150					155					160	
Arg	Val	Thr	Ile	Leu	Val	Glu	Gly	Gly	Glu	Ile	Glu	Leu	Phe	Asp	Gly
			165					170						175	
Glu	Val	Asn	Val	Lys	Arg	Pro	Met	Lys	Asp	Glu	Thr	His	Phe	Glu	Val
			180					185					190		
Val	Glu	Ser	Gly	Arg	Tyr	Ile	Ile	Leu	Leu	Leu	Gly	Lys	Ala	Leu	Ser
			195				200					205			
Val	Val	Trp	Asp	Arg	His	Leu	Ser	Ile	Ser	Val	Val	Leu	Lys	Gln	Thr
			210			215					220				
Tyr	Gln	Glu	Lys	Val	Cys	Gly	Leu	Cys	Gly	Asn	Phe	Asp	Gly	Ile	Gln
225				230					235					240	
Asn	Asn	Asp	Leu	Thr	Ser	Ser	Asn	Leu	Gln	Val	Glu	Glu	Asp	Pro	Val
			245					250						255	
Asp	Phe	Gly	Asn	Ser	Trp	Lys	Val	Ser	Ser	Gln	Cys	Ala	Asp	Thr	Arg
			260				265						270		
Lys	Val	Pro	Leu	Asp	Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met
			275				280					285			
Lys	Gln	Thr	Met	Val	Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val
			290			295					300				
Phe	Gln	Asp	Cys	Asn	Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val
305				310					315					320	
Cys	Ile	Tyr	Asp	Thr	Cys	Ser	Cys	Glu	Ser	Ile	Gly	Asp	Cys	Ala	Cys
			325					330					335		
Phe	Cys	Asp	Thr	Ile	Ala	Ala	Tyr	Ala	His	Val	Cys	Ala	Gln	His	Gly
			340				345						350		

Lys	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu	
355 360 365															
Glu	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn
370 375 380															
Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu
385 390 395 400															
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro
405 410 415															
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp
420 425 430															
Cys	Pro	Val	Cys	Glu	Val	Ala	Gly	Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys
435 440 445															
Val	Thr	Leu	Asn	Pro	Ser	Asp	Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys
450 455 460															
Asp	Val	Val	Asn	Leu	Thr	Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	Leu
465 470 475 480															
Val	Val	Pro	Pro	Thr	Asp	Ala									
485															
<210> SEQ ID NO 12															
<211> LENGTH: 386															
<212> TYPE: PRT															
<213> ORGANISM: Artificial Sequence															
<220> FEATURE:															
<223> OTHER INFORMATION: vWF fragment: amino acids 864-1250 (D3 I)															
<400> SEQUENCE: 12															
Ala	Thr	Cys	Ser	Thr	Ile	Gly	Met	Ala	His	Tyr	Leu	Thr	Phe	Asp	Gly
1	5 10 15														
Leu	Lys	Tyr	Leu	Phe	Pro	Gly	Glu	Cys	Gln	Tyr	Val	Leu	Val	Gln	Asp
20 25 30															
Tyr	Cys	Gly	Ser	Asn	Pro	Gly	Thr	Phe	Arg	Ile	Leu	Val	Gly	Asn	Lys
35 40 45															
Gly	Cys	Ser	His	Pro	Ser	Val	Lys	Cys	Lys	Lys	Arg	Val	Thr	Ile	Leu
50 55 60															
Val	Glu	Gly	Gly	Glu	Ile	Glu	Leu	Phe	Asp	Gly	Glu	Val	Asn	Val	Lys
65 70 75 80															
Arg	Pro	Met	Lys	Asp	Glu	Thr	His	Phe	Glu	Val	Val	Glu	Ser	Gly	Arg
85 90 95															
Tyr	Ile	Ile	Leu	Leu	Leu	Gly	Lys	Ala	Leu	Ser	Val	Val	Trp	Asp	Arg
100 105 110															
His	Leu	Ser	Ile	Ser	Val	Val	Leu	Lys	Gln	Thr	Tyr	Gln	Glu	Lys	Val
115 120 125															
Cys	Gly	Leu	Cys	Gly	Asn	Phe	Asp	Gly	Ile	Gln	Asn	Asn	Asp	Leu	Thr
130 135 140															
Ser	Ser	Asn	Leu	Gln	Val	Glu	Glu	Asp	Pro	Val	Asp	Phe	Gly	Asn	Ser
145 150 155 160															
Trp	Lys	Val	Ser	Ser	Gln	Cys	Ala	Asp	Thr	Arg	Lys	Val	Pro	Leu	Asp
165 170 175															
Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met	Lys	Gln	Thr	Met	Val
180 185 190															
Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val	Phe	Gln	Asp	Cys	Asn
195 200 205															
Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val	Cys	Ile	Tyr	Asp	Thr
210 215 220															

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Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys Phe Cys Asp Thr Ile
 225 230 235 240
 Ala Ala Tyr Ala His Val Cys Ala Gln His Gly Lys Val Val Thr Trp
 245 250 255
 Arg Thr Ala Thr Leu Cys Pro Gln Ser Cys Glu Glu Arg Asn Leu Arg
 260 265 270
 Glu Asn Gly Tyr Glu Cys Glu Trp Arg Tyr Asn Ser Cys Ala Pro Ala
 275 280 285
 Cys Gln Val Thr Cys Gln His Pro Glu Pro Leu Ala Cys Pro Val Gln
 290 295 300
 Cys Val Glu Gly Cys His Ala His Cys Pro Pro Gly Lys Ile Leu Asp
 305 310 315 320
 Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp Cys Pro Val Cys Glu
 325 330 335
 Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys Val Thr Leu Asn Pro
 340 345 350
 Ser Asp Pro Glu His Cys Gln Ile Cys His Cys Asp Val Val Asn Leu
 355 360 365
 Thr Cys Glu Ala Cys Gln Glu Pro Gly Gly Leu Val Val Pro Pro Thr
 370 375 380
 Asp Ala
 385

<210> SEQ ID NO 13
 <211> LENGTH: 405
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: vWF fragment: amino acids 864-1268 (D3 II)
 <400> SEQUENCE: 13

Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
 1 5 10 15
 Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
 20 25 30
 Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
 35 40 45
 Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
 50 55 60
 Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
 65 70 75 80
 Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
 85 90 95
 Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
 100 105 110
 His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
 115 120 125
 Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln Asn Asn Asp Leu Thr
 130 135 140
 Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val Asp Phe Gly Asn Ser
 145 150 155 160
 Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg Lys Val Pro Leu Asp
 165 170 175
 Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met Lys Gln Thr Met Val
 180 185 190

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Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val Phe Gln Asp Cys Asn
 195 200 205
 Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val Cys Ile Tyr Asp Thr
 210 215 220
 Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys Phe Cys Asp Thr Ile
 225 230 235 240
 Ala Ala Tyr Ala His Val Cys Ala Gln His Gly Lys Val Val Thr Trp
 245 250 255
 Arg Thr Ala Thr Leu Cys Pro Gln Ser Cys Glu Glu Arg Asn Leu Arg
 260 265 270
 Glu Asn Gly Tyr Glu Cys Glu Trp Arg Tyr Asn Ser Cys Ala Pro Ala
 275 280 285
 Cys Gln Val Thr Cys Gln His Pro Glu Pro Leu Ala Cys Pro Val Gln
 290 295 300
 Cys Val Glu Gly Cys His Ala His Cys Pro Pro Gly Lys Ile Leu Asp
 305 310 315 320
 Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp Cys Pro Val Cys Glu
 325 330 335
 Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys Val Thr Leu Asn Pro
 340 345 350
 Ser Asp Pro Glu His Cys Gln Ile Cys His Cys Asp Val Val Asn Leu
 355 360 365
 Thr Cys Glu Ala Cys Gln Glu Pro Gly Gly Leu Val Val Pro Pro Thr
 370 375 380
 Asp Ala Pro Val Ser Pro Thr Thr Leu Tyr Val Glu Asp Ile Ser Glu
 385 390 395 400
 Pro Pro Leu His Asp
 405

<210> SEQ ID NO 14
 <211> LENGTH: 498
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: vWF fragment: amino acids 764-1261
 (TIL'/E'/D3 II)

<400> SEQUENCE: 14

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
 1 5 10 15
 Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
 20 25 30
 Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
 35 40 45
 Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
 50 55 60
 Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
 65 70 75 80
 Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
 85 90 95
 Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
 100 105 110
 Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
 115 120 125
 Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile

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130	135	140
Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys		
145	150	155 160
Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly		
	165	170 175
Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val		
	180	185 190
Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser		
	195	200 205
Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr		
	210	215 220
Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln		
	225	230 235 240
Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val		
	245	250 255
Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg		
	260	265 270
Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met		
	275	280 285
Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val		
	290	295 300
Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val		
	305	310 315 320
Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys		
	325	330 335
Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln His Gly		
	340	345 350
Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln Ser Cys Glu		
	355	360 365
Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu Cys Glu Trp Arg Tyr Asn		
	370	375 380
Ser Cys Ala Pro Ala Cys Gln Val Thr Cys Gln His Pro Glu Pro Leu		
	385	390 395 400
Ala Cys Pro Val Gln Cys Val Glu Gly Cys His Ala His Cys Pro Pro		
	405	410 415
Gly Lys Ile Leu Asp Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp		
	420	425 430
Cys Pro Val Cys Glu Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys		
	435	440 445
Val Thr Leu Asn Pro Ser Asp Pro Glu His Cys Gln Ile Cys His Cys		
	450	455 460
Asp Val Val Asn Leu Thr Cys Glu Ala Cys Gln Glu Pro Gly Gly Leu		
	465	470 475 480
Val Val Pro Pro Thr Asp Ala Pro Val Ser Pro Thr Thr Leu Tyr Val		
	485	490 495
Glu Asp		

<210> SEQ ID NO 15

<211> LENGTH: 502

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: vWF fragment: amino acids 764-1264
(TIL'/E'/D3 III)

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<400> SEQUENCE: 15

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
 1 5 10 15
 Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
 20 25 30
 Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
 35 40 45
 Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
 50 55 60
 Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
 65 70 75 80
 Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
 85 90 95
 Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
 100 105 110
 Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
 115 120 125
 Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
 130 135 140
 Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
 145 150 155 160
 Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
 165 170 175
 Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
 180 185 190
 Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser
 195 200 205
 Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr
 210 215 220
 Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln
 225 230 235 240
 Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val
 245 250 255
 Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg
 260 265 270
 Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met
 275 280 285
 Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val
 290 295 300
 Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val
 305 310 315 320
 Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys
 325 330 335
 Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln His Gly
 340 345 350
 Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln Ser Cys Glu
 355 360 365
 Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu Cys Glu Trp Arg Tyr Asn
 370 375 380
 Ser Cys Ala Pro Ala Cys Gln Val Thr Cys Gln His Pro Glu Pro Leu
 385 390 395 400
 Ala Cys Pro Val Gln Cys Val Glu Gly Cys His Ala His Cys Pro Pro
 405 410 415

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Gly Lys Ile Leu Asp Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp
 420 425 430
 Cys Pro Val Cys Glu Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys
 435 440 445
 Val Thr Leu Asn Pro Ser Asp Pro Glu His Cys Gln Ile Cys His Cys
 450 455 460
 Asp Val Val Asn Leu Thr Cys Glu Ala Cys Gln Glu Pro Gly Gly Leu
 465 470 475 480
 Val Val Pro Pro Thr Asp Ala Pro Val Ser Pro Thr Thr Leu Tyr Val
 485 490 495
 Glu Asp Ile Ser Glu Pro
 500

<210> SEQ ID NO 16
 <211> LENGTH: 506
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: vWF fragment: amino acids 764-1268
 (TIL'/E'/D3 IV)

<400> SEQUENCE: 16

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
 1 5 10 15
 Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
 20 25 30
 Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
 35 40 45
 Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
 50 55 60
 Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
 65 70 75 80
 Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
 85 90 95
 Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
 100 105 110
 Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
 115 120 125
 Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
 130 135 140
 Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
 145 150 155 160
 Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
 165 170 175
 Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
 180 185 190
 Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser
 195 200 205
 Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr
 210 215 220
 Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln
 225 230 235 240
 Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val
 245 250 255
 Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg

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260					265					270					
Lys	Val	Pro	Leu	Asp	Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met
	275						280					285			
Lys	Gln	Thr	Met	Val	Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val
	290					295					300				
Phe	Gln	Asp	Cys	Asn	Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val
	305					310					315				320
Cys	Ile	Tyr	Asp	Thr	Cys	Ser	Cys	Glu	Ser	Ile	Gly	Asp	Cys	Ala	Cys
				325					330					335	
Phe	Cys	Asp	Thr	Ile	Ala	Ala	Tyr	Ala	His	Val	Cys	Ala	Gln	His	Gly
			340					345					350		
Lys	Val	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu
		355					360					365			
Glu	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn
	370					375					380				
Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu
	385					390					395				400
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro
			405						410					415	
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp
		420						425					430		
Cys	Pro	Val	Cys	Glu	Val	Ala	Gly	Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys
		435					440					445			
Val	Thr	Leu	Asn	Pro	Ser	Asp	Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys
	450					455					460				
Asp	Val	Val	Asn	Leu	Thr	Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	Leu
	465					470					475				480
Val	Val	Pro	Pro	Thr	Asp	Ala	Pro	Val	Ser	Pro	Thr	Thr	Leu	Tyr	Val
			485					490					495		
Glu	Asp	Ile	Ser	Glu	Pro	Pro	Leu	His	Asp						
		500					505								

<210> SEQ ID NO 17

<211> LENGTH: 696

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: vWF fragment: amino acids 764-1459

(TIL'/E'/D3/A1 I)

<400> SEQUENCE: 17

Ser	Leu	Ser	Cys	Arg	Pro	Pro	Met	Val	Lys	Leu	Val	Cys	Pro	Ala	Asp
1				5					10					15	
Asn	Leu	Arg	Ala	Glu	Gly	Leu	Glu	Cys	Thr	Lys	Thr	Cys	Gln	Asn	Tyr
			20					25					30		
Asp	Leu	Glu	Cys	Met	Ser	Met	Gly	Cys	Val	Ser	Gly	Cys	Leu	Cys	Pro
		35					40					45			
Pro	Gly	Met	Val	Arg	His	Glu	Asn	Arg	Cys	Val	Ala	Leu	Glu	Arg	Cys
		50				55					60				
Pro	Cys	Phe	His	Gln	Gly	Lys	Glu	Tyr	Ala	Pro	Gly	Glu	Thr	Val	Lys
	65				70				75					80	
Ile	Gly	Cys	Asn	Thr	Cys	Val	Cys	Gln	Asp	Arg	Lys	Trp	Asn	Cys	Thr
			85					90					95		
Asp	His	Val	Cys	Asp	Ala	Thr	Cys	Ser	Thr	Ile	Gly	Met	Ala	His	Tyr
			100				105						110		

Leu	Thr	Phe	Asp	Gly	Leu	Lys	Tyr	Leu	Phe	Pro	Gly	Glu	Cys	Gln	Tyr
		115					120					125			
Val	Leu	Val	Gln	Asp	Tyr	Cys	Gly	Ser	Asn	Pro	Gly	Thr	Phe	Arg	Ile
	130					135					140				
Leu	Val	Gly	Asn	Lys	Gly	Cys	Ser	His	Pro	Ser	Val	Lys	Cys	Lys	Lys
	145				150					155					160
Arg	Val	Thr	Ile	Leu	Val	Glu	Gly	Gly	Glu	Ile	Glu	Leu	Phe	Asp	Gly
				165					170					175	
Glu	Val	Asn	Val	Lys	Arg	Pro	Met	Lys	Asp	Glu	Thr	His	Phe	Glu	Val
			180					185					190		
Val	Glu	Ser	Gly	Arg	Tyr	Ile	Ile	Leu	Leu	Leu	Gly	Lys	Ala	Leu	Ser
		195					200					205			
Val	Val	Trp	Asp	Arg	His	Leu	Ser	Ile	Ser	Val	Val	Leu	Lys	Gln	Thr
	210					215					220				
Tyr	Gln	Glu	Lys	Val	Cys	Gly	Leu	Cys	Gly	Asn	Phe	Asp	Gly	Ile	Gln
	225				230					235					240
Asn	Asn	Asp	Leu	Thr	Ser	Ser	Asn	Leu	Gln	Val	Glu	Glu	Asp	Pro	Val
				245					250					255	
Asp	Phe	Gly	Asn	Ser	Trp	Lys	Val	Ser	Ser	Gln	Cys	Ala	Asp	Thr	Arg
			260					265					270		
Lys	Val	Pro	Leu	Asp	Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met
		275					280					285			
Lys	Gln	Thr	Met	Val	Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val
	290				295						300				
Phe	Gln	Asp	Cys	Asn	Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val
	305				310					315					320
Cys	Ile	Tyr	Asp	Thr	Cys	Ser	Cys	Glu	Ser	Ile	Gly	Asp	Cys	Ala	Cys
				325				330						335	
Phe	Cys	Asp	Thr	Ile	Ala	Ala	Tyr	Ala	His	Val	Cys	Ala	Gln	His	Gly
			340					345					350		
Lys	Val	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu
	355					360						365			
Glu	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn
	370				375						380				
Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu
	385				390					395					400
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro
				405					410					415	
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp
			420					425					430		
Cys	Pro	Val	Cys	Glu	Val	Ala	Gly	Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys
	435					440						445			
Val	Thr	Leu	Asn	Pro	Ser	Asp	Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys
	450					455					460				
Asp	Val	Val	Asn	Leu											

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530	535	540
Arg Ile Ser Gln Lys Trp Val Arg Val Ala Val Val Glu Tyr His Asp		
545	550	555 560
Gly Ser His Ala Tyr Ile Gly Leu Lys Asp Arg Lys Arg Pro Ser Glu		
	565	570 575
Leu Arg Arg Ile Ala Ser Gln Val Lys Tyr Ala Gly Ser Gln Val Ala		
	580	585 590
Ser Thr Ser Glu Val Leu Lys Tyr Thr Leu Phe Gln Ile Phe Ser Lys		
	595	600 605
Ile Asp Arg Pro Glu Ala Ser Arg Ile Thr Leu Leu Leu Met Ala Ser		
610	615	620
Gln Glu Pro Gln Arg Met Ser Arg Asn Phe Val Arg Tyr Val Gln Gly		
625	630	635 640
Leu Lys Lys Lys Lys Val Ile Val Ile Pro Val Gly Ile Gly Pro His		
	645	650 655
Ala Asn Leu Lys Gln Ile Arg Leu Ile Glu Lys Gln Ala Pro Glu Asn		
	660	665 670
Lys Ala Phe Val Leu Ser Ser Val Asp Glu Leu Glu Gln Gln Arg Asp		
	675	680 685
Glu Ile Val Ser Tyr Leu Cys Asp		
690	695	

<210> SEQ ID NO 18
 <211> LENGTH: 700
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: vWF fragment: amino acids 764-1463
 (TIL'/E'/D3/A1 II)

<400> SEQUENCE: 18

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
1 5 10 15
Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
20 25 30
Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
35 40 45
Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
50 55 60
Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
65 70 75 80
Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
85 90 95
Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
100 105 110
Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
115 120 125
Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
130 135 140
Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
145 150 155 160
Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
165 170 175
Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
180 185 190

Val 195	Glu	Ser	Gly	Arg	Tyr	Ile	Ile	Leu	Leu	Leu	Gly	Lys	Ala	Leu	Ser
Val 210	Val	Trp	Asp	Arg	His	Leu	Ser	Ile	Ser	Val	Val	Leu	Lys	Gln	Thr
Tyr 225	Gln	Glu	Lys	Val	Cys	Gly	Leu	Cys	Gly	Asn	Phe	Asp	Gly	Ile	Gln
Asn	Asn	Asp	Leu	Thr	Ser	Ser	Asn	Leu	Gln	Val	Glu	Glu	Asp	Pro	Val
Asp	Phe	Gly	Asn	Ser	Trp	Lys	Val	Ser	Ser	Gln	Cys	Ala	Asp	Thr	Arg
Lys	Val	Pro	Leu	Asp	Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met
Lys	Gln	Thr	Met	Val	Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val
Phe 305	Gln	Asp	Cys	Asn	Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val
Cys	Ile	Tyr	Asp	Thr	Cys	Ser	Cys	Glu	Ser	Ile	Gly	Asp	Cys	Ala	Cys
Phe	Cys	Asp	Thr	Ile	Ala	Ala	Tyr	Ala	His	Val	Cys	Ala	Gln	His	Gly
Lys	Val	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu
Glu 370	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn
Ser 385	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp
Cys	Pro	Val	Cys	Glu	Val	Ala	Gly	Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys
Val 450	Thr	Leu	Asn	Pro	Ser	Asp	Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys
Asp 465	Val	Val	Asn	Leu	Thr	Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	Leu
Val	Val	Pro	Pro	Thr	Asp	Ala	Pro	Val	Ser	Pro	Thr	Thr	Leu	Tyr	Val
Glu	Asp	Ile	Ser	Glu	Pro	Pro	Leu	His	Asp	Phe	Tyr	Cys	Ser	Arg	Leu
Leu	Asp	Leu	Val	Phe	Leu	Leu	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Glu	Ala
Glu 530	Phe	Glu	Val	Leu	Lys	Ala	Phe	Val	Val	Asp	Met	Met	Glu	Arg	Leu
Arg 545	Ile	Ser	Gln	Lys	Trp	Val	Arg	Val	Ala	Val	Val	Glu	Tyr	His	Asp
Gly	Ser	His	Ala	Tyr	Ile	Gly	Leu	Lys	Asp	Arg	Lys	Arg	Pro	Ser	Glu
Leu	Arg	Arg	Ile	Ala	Ser	Gln	Val	Lys	Tyr	Ala	Gly	Ser	Gln	Val	Ala
Ser	Thr	Ser	Glu	Val	Leu	Lys	Tyr	Thr	Leu	Phe	Gln	Ile	Phe	Ser	Lys
Ile	Asp	Arg	Pro	Glu	Ala	Ser	Arg	Ile	Thr	Leu	Leu	Leu	Met	Ala	Ser

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610	615	620
Gln Glu Pro Gln Arg Met Ser Arg Asn Phe Val Arg Tyr Val Gln Gly		
625	630	635 640
Leu Lys Lys Lys Lys Val Ile Val Ile Pro Val Gly Ile Gly Pro His		
	645	650 655
Ala Asn Leu Lys Gln Ile Arg Leu Ile Glu Lys Gln Ala Pro Glu Asn		
	660	665 670
Lys Ala Phe Val Leu Ser Ser Val Asp Glu Leu Glu Gln Gln Arg Asp		
	675	680 685
Glu Ile Val Ser Tyr Leu Cys Asp Leu Ala Pro Glu		
690	695	700

<210> SEQ ID NO 19
 <211> LENGTH: 701
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: vWF fragment: amino acids 764-1464
 (TIL'/E'/D3/A1 III)

<400> SEQUENCE: 19

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
1 5 10 15
Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
20 25 30
Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
35 40 45
Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys
50 55 60
Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys
65 70 75 80
Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr
85 90 95
Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr
100 105 110
Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr
115 120 125
Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile
130 135 140
Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys
145 150 155 160
Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly
165 170 175
Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val
180 185 190
Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser
195 200 205
Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr
210 215 220
Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln
225 230 235 240
Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val
245 250 255
Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg
260 265 270

Lys	Val	Pro	Leu	Asp	Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met
275						280				285					
Lys	Gln	Thr	Met	Val	Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val
290						295				300					
Phe	Gln	Asp	Cys	Asn	Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val
305				310				330		315				320	
Cys	Ile	Tyr	Asp	Thr	Cys	Ser	Cys	Glu	Ser	Ile	Gly	Asp	Cys	Ala	Cys
				325				345						335	
Phe	Cys	Asp	Thr	Ile	Ala	Ala	Tyr	Ala	His	Val	Cys	Ala	Gln	His	Gly
		340						360				350			
Lys	Val	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu
355						360						365			
Glu	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn
370						375				380					
Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu
385				390						395				400	
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro
				405				410						415	
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp
		420						425				430			
Cys	Pro	Val	Cys	Glu	Val	Ala	Gly	Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys
435						440						445			
Val	Thr	Leu	Asn	Pro	Ser	Asp	Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys
450						455				460					
Asp	Val	Val	Asn	Leu	Thr	Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	Leu
465				470						475				480	
Val	Val	Pro	Pro	Thr	Asp	Ala	Pro	Val	Ser	Pro	Thr	Thr	Leu	Tyr	Val
				485				490						495	
Glu	Asp	Ile	Ser	Glu	Pro	Pro	Leu	His	Asp	Phe	Tyr	Cys	Ser	Arg	Leu
		500						505				510			
Leu	Asp	Leu	Val	Phe	Leu	Leu	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Glu	Ala
515						520						525			
Glu	Phe	Glu	Val	Leu	Lys	Ala	Phe	Val	Val	Asp	Met	Met	Glu	Arg	Leu
530				535						540					
Arg	Ile	Ser	Gln	Lys	Trp	Val	Arg	Val	Ala	Val	Val	Glu	Tyr	His	Asp
545				550						555				560	
Gly	Ser	His	Ala	Tyr	Ile	Gly	Leu	Lys	Asp	Arg	Lys	Arg	Pro	Ser	Glu
				565				570						575	
Leu	Arg	Arg	Ile	Ala	Ser	Gln	Val	Lys	Tyr	Ala	Gly	Ser	Gln	Val	Ala
		580						585				590			
Ser	Thr	Ser	Glu	Val	Leu	Lys	Tyr	Thr	Leu	Phe	Gln	Ile	Phe	Ser	Lys
595						600						605			
Ile	Asp	Arg	Pro	Glu	Ala	Ser	Arg	Ile	Thr	Leu	Leu	Leu	Met	Ala	Ser
610						615				620					
Gln	Glu	Pro	Gln	Arg	Met	Ser	Arg	Asn	Phe	Val	Arg	Tyr	Val	Gln	Gly
625				630						635				640	
Leu	Lys	Lys	Lys</												

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690	695	700
<210> SEQ ID NO 20		
<211> LENGTH: 920		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: vWF fragment: amino acids 764-1683		
(TIL'/E'/D3/A1/A2)		
<400> SEQUENCE: 20		
Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp		
1 5 10 15		
Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr		
20 25 30		
Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro		
35 40 45		
Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys		
50 55 60		
Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys		
65 70 75 80		
Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr		
85 90 95		
Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr		
100 105 110		
Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr		
115 120 125		
Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile		
130 135 140		
Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys		
145 150 155 160		
Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly		
165 170 175		
Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val		
180 185 190		
Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser		
195 200 205		
Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr		
210 215 220		
Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln		
225 230 235 240		
Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val		
245 250 255		
Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg		
260 265 270		
Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met		
275 280 285		
Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val		
290 295 300		
Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val		
305 310 315 320		
Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys		
325 330 335		
Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln His Gly		
340 345 350		

Lys	Val	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu
355							360					365			
Glu	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn
370						375					380				
Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu
385					390					395					400
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro
			405						410					415	
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp
			420					425					430		
Cys	Pro	Val	Cys	Glu	Val	Ala	Gly	Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys
435							440					445			
Val	Thr	Leu	Asn	Pro	Ser	Asp	Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys
450						455					460				
Asp	Val	Val	Asn	Leu	Thr	Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	Leu
465					470					475					480
Val	Val	Pro	Pro	Thr	Asp	Ala	Pro	Val	Ser	Pro	Thr	Thr	Leu	Tyr	Val
			485						490					495	
Glu	Asp	Ile	Ser	Glu	Pro	Pro	Leu	His	Asp	Phe	Tyr	Cys	Ser	Arg	Leu
			500					505					510		
Leu	Asp	Leu	Val	Phe	Leu	Leu	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Glu	Ala
515							520					525			
Glu	Phe	Glu	Val	Leu	Lys	Ala	Phe	Val	Val	Asp	Met	Met	Glu	Arg	Leu
530					535						540				
Arg	Ile	Ser	Gln	Lys	Trp	Val	Arg	Val	Ala	Val	Val	Glu	Tyr	His	Asp
545					550					555					560
Gly	Ser	His	Ala	Tyr	Ile	Gly	Leu	Lys	Asp	Arg	Lys	Arg	Pro	Ser	Glu
			565					570						575	
Leu	Arg	Arg	Ile	Ala	Ser	Gln	Val	Lys	Tyr	Ala	Gly	Ser	Gln	Val	Ala
			580					585					590		
Ser	Thr	Ser	Glu	Val	Leu	Lys	Tyr	Thr	Leu	Phe	Gln	Ile	Phe	Ser	Lys
595						600						605			
Ile	Asp	Arg	Pro	Glu	Ala	Ser	Arg	Ile	Thr	Leu	Leu	Leu	Met	Ala	Ser
610						615					620				
Gln	Glu	Pro	Gln	Arg	Met	Ser	Arg	Asn	Phe	Val	Arg	Tyr	Val	Gln	Gly
625					630					635					640
Leu	Lys	Lys	Lys	Lys	Val	Ile	Val	Ile	Pro	Val	Gly	Ile	Gly	Pro	His
			645					650					655		
Ala	Asn	Leu	Lys	Gln	Ile	Arg	Leu	Ile	Glu	Lys	Gln	Ala	Pro	Glu	Asn
660							665					670			
Lys	Ala	Phe	Val	Leu	Ser	Ser	Val	Asp	Glu	Leu	Glu	Gln	Gln	Arg	Asp
675						680						685			
Glu	Ile	Val	Ser	Tyr	Leu	Cys	Asp	Leu	Ala	Pro	Glu	Ala	Pro	Pro	Pro
690						695					700				
Thr	Leu	Pro	Pro	Asp	Met	Ala	Gln	Val	Thr	Val	Gly	Pro	Gly	Leu	Leu
705					7										

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770	775	780
Val Glu Tyr Pro Phe Ser Glu Ala Gln Ser Lys Gly Asp Ile Leu Gln		
785	790	795 800
Arg Val Arg Glu Ile Arg Tyr Gln Gly Gly Asn Arg Thr Asn Thr Gly		
	805	810 815
Leu Ala Leu Arg Tyr Leu Ser Asp His Ser Phe Leu Val Ser Gln Gly		
	820	825 830
Asp Arg Glu Gln Ala Pro Asn Leu Val Tyr Met Val Thr Gly Asn Pro		
	835	840 845
Ala Ser Asp Glu Ile Lys Arg Leu Pro Gly Asp Ile Gln Val Val Pro		
	850	855 860
Ile Gly Val Gly Pro Asn Ala Asn Val Gln Glu Leu Glu Arg Ile Gly		
	865	870 875 880
Trp Pro Asn Ala Pro Ile Leu Ile Gln Asp Phe Glu Thr Leu Pro Arg		
	885	890 895
Glu Ala Pro Asp Leu Val Leu Gln Arg Cys Cys Ser Gly Glu Gly Leu		
	900	905 910
Gln Ile Pro Thr Leu Ser Pro Ala		
	915	920

<210> SEQ ID NO 21

<211> LENGTH: 1110

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: vWF fragment: amino acids 764-1873

(TIL'/E'/D3/A1/A2/A3)

<400> SEQUENCE: 21

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp		
1	5	10 15
Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr		
	20	25 30
Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro		
	35	40 45
Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys		
	50	55 60
Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys		
	65	70 75 80
Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr		
	85	90 95
Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr		
	100	105 110
Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr		
	115	120 125
Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile		
	130	135 140
Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys		
	145	150 155 160
Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly		
	165	170 175
Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val		
	180	185 190
Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser		
	195	200 205

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Val	Val	Trp	Asp	Arg	His	Leu	Ser	Ile	Ser	Val	Val	Leu	Lys	Gln	Thr
210						215				220					
Tyr	Gln	Glu	Lys	Val	Cys	Gly	Leu	Cys	Gly	Asn	Phe	Asp	Gly	Ile	Gln
225					230					235					240
Asn	Asn	Asp	Leu	Thr	Ser	Ser	Asn	Leu	Gln	Val	Glu	Glu	Asp	Pro	Val
			245						250					255	
Asp	Phe	Gly	Asn	Ser	Trp	Lys	Val	Ser	Ser	Gln	Cys	Ala	Asp	Thr	Arg
		260						265					270		
Lys	Val	Pro	Leu	Asp	Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met
		275					280					285			
Lys	Gln	Thr	Met	Val	Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val
	290					295					300				
Phe	Gln	Asp	Cys	Asn	Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val
305					310					315					320
Cys	Ile	Tyr	Asp	Thr	Cys	Ser	Cys	Glu	Ser	Ile	Gly	Asp	Cys	Ala	Cys
			325						330					335	
Phe	Cys	Asp	Thr	Ile	Ala	Ala	Tyr	Ala	His	Val	Cys	Ala	Gln	His	Gly
		340						345					350		
Lys	Val	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu
		355					360					365			
Glu	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn
	370					375					380				
Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu
385					390					395					400
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro
			405						410					415	
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp
			420					425					430		
Cys	Pro	Val	Cys	Glu	Val	Ala	Gly	Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys
		435					440					445			
Val	Thr	Leu	Asn	Pro	Ser	Asp	Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys
	450					455					460				
Asp	Val	Val	Asn	Leu	Thr	Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	Leu
465					470					475					480
Val	Val	Pro	Pro	Thr	Asp	Ala	Pro	Val	Ser	Pro	Thr	Thr	Leu	Tyr	Val
				485					490					495	
Glu	Asp	Ile	Ser	Glu	Pro	Pro	Leu	His	Asp	Phe	Tyr	Cys	Ser	Arg	Leu
			500					505				510			
Leu	Asp	Leu	Val	Phe	Leu	Leu	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Glu	Ala
		515					520					525			
Glu	Phe	Glu	Val	Leu	Lys	Ala	Phe	Val	Val	Asp	Met	Met	Glu	Arg	Leu
	530					535					540				
Arg	Ile	Ser	Gln	Lys	Trp	Val	Arg	Val	Ala	Val	Val	Glu	Tyr	His	Asp
545					550					555					560
Gly	Ser	His	Ala	Tyr	Ile	Gly	Leu	Lys	Asp	Arg	Lys	Arg	Pro	Ser	Glu
			565						570					575	
Leu	Arg	Arg	Ile	Ala	Ser	Gln	Val	Lys	Tyr	Ala	Gly	Ser	Gln	Val	Ala
			580					585					590		
Ser	Thr	Ser	Glu	Val	Leu	Lys	Tyr	Thr	Leu	Phe	Gln	Ile	Phe	Ser	Lys
		595					600					605			
Ile	Asp	Arg	Pro	Glu	Ala	Ser	Arg	Ile	Thr	Leu	Leu	Leu	Met	Ala	Ser
	610					615				620					
Gln	Glu	Pro	Gln	Arg	Met	Ser	Arg	Asn	Phe	Val	Arg	Tyr	Val	Gln	Gly

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625	630	635	640
Leu Lys Lys Lys Lys Val Ile Val Ile Pro Val Gly Ile Gly Pro His			
	645	650	655
Ala Asn Leu Lys Gln Ile Arg Leu Ile Glu Lys Gln Ala Pro Glu Asn			
	660	665	670
Lys Ala Phe Val Leu Ser Ser Val Asp Glu Leu Glu Gln Gln Arg Asp			
	675	680	685
Glu Ile Val Ser Tyr Leu Cys Asp Leu Ala Pro Glu Ala Pro Pro Pro			
	690	695	700
Thr Leu Pro Pro Asp Met Ala Gln Val Thr Val Gly Pro Gly Leu Leu			
	705	710	715
Gly Val Ser Thr Leu Gly Pro Lys Arg Asn Ser Met Val Leu Asp Val			
	725	730	735
Ala Phe Val Leu Glu Gly Ser Asp Lys Ile Gly Glu Ala Asp Phe Asn			
	740	745	750
Arg Ser Lys Glu Phe Met Glu Glu Val Ile Gln Arg Met Asp Val Gly			
	755	760	765
Gln Asp Ser Ile His Val Thr Val Leu Gln Tyr Ser Tyr Met Val Thr			
	770	775	780
Val Glu Tyr Pro Phe Ser Glu Ala Gln Ser Lys Gly Asp Ile Leu Gln			
	785	790	795
Arg Val Arg Glu Ile Arg Tyr Gln Gly Gly Asn Arg Thr Asn Thr Gly			
	805	810	815
Leu Ala Leu Arg Tyr Leu Ser Asp His Ser Phe Leu Val Ser Gln Gly			
	820	825	830
Asp Arg Glu Gln Ala Pro Asn Leu Val Tyr Met Val Thr Gly Asn Pro			
	835	840	845
Ala Ser Asp Glu Ile Lys Arg Leu Pro Gly Asp Ile Gln Val Val Pro			
	850	855	860
Ile Gly Val Gly Pro Asn Ala Asn Val Gln Glu Leu Glu Arg Ile Gly			
	865	870	875
Trp Pro Asn Ala Pro Ile Leu Ile Gln Asp Phe Glu Thr Leu Pro Arg			
	885	890	895
Glu Ala Pro Asp Leu Val Leu Gln Arg Cys Cys Ser Gly Glu Gly Leu			
	900	905	910
Gln Ile Pro Thr Leu Ser Pro Ala Pro Asp Cys Ser Gln Pro Leu Asp			
	915	920	925
Val Ile Leu Leu Leu Asp Gly Ser Ser Ser Phe Pro Ala Ser Tyr Phe			
	930	935	940
Asp Glu Met Lys Ser Phe Ala Lys Ala Phe Ile Ser Lys Ala Asn Ile			
	945	950	955
Gly Pro Arg Leu Thr Gln Val Ser Val Leu Gln Tyr Gly Ser Ile Thr			
	965	970	975
Thr Ile Asp Val Pro Trp Asn Val Val Pro Glu Lys Ala His Leu Leu			
	980	985	990
Ser Leu Val Asp Val Met Gln Arg Glu Gly Gly Pro Ser Gln Ile Gly			
	995	1000	1005
Asp Ala Leu Gly Phe Ala Val Arg Tyr Leu Thr Ser Glu Met His			
	1010	1015	1020
Gly Ala Arg Pro Gly Ala Ser Lys Ala Val Val Ile Leu Val Thr			
	1025	1030	1035
Asp Val Ser Val Asp Ser Val Asp Ala Ala Ala Asp Ala Ala Arg			
	1040	1045	1050

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Ser Asn  Arg Val Thr Val Phe  Pro Ile Gly Ile Gly  Asp Arg Tyr
1055                                1060                    1065

Asp Ala  Ala Gln Leu Arg Ile  Leu Ala Gly Pro Ala  Gly Asp Ser
1070                                1075                    1080

Asn Val  Val Lys Leu Gln Arg  Ile Glu Asp Leu Pro  Thr Met Val
1085                                1090                    1095

Thr Leu  Gly Asn Ser Phe Leu  His Lys Leu Cys Ser
1100                                1105                    1110

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<210> SEQ ID NO 22
<211> LENGTH: 2813
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

```

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<400> SEQUENCE: 22

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Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1           5           10           15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr
20          25          30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
35          40          45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
50          55          60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65          70          75          80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
85          90          95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
100         105         110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
115         120         125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
130         135         140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145         150         155         160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
165         170         175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
180         185         190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
195         200         205

Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
210         215         220

Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225         230         235         240

Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
245         250         255

Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
260         265         270

Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
275         280         285

Ser Ala Cys Ser Pro Val Cys Pro Ala Gly Met Glu Tyr Arg Gln Cys
290         295         300

Val Ser Pro Cys Ala Arg Thr Cys Gln Ser Leu His Ile Asn Glu Met

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305	310							315							320		
Cys	Gln	Glu	Arg	Cys	Val	Asp	Gly	Cys	Ser	Cys	Pro	Glu	Gly	Gln	Leu		
				325					330					335			
Leu	Asp	Glu	Gly	Leu	Cys	Val	Glu	Ser	Thr	Glu	Cys	Pro	Cys	Val	His		
			340					345					350				
Ser	Gly	Lys	Arg	Tyr	Pro	Pro	Gly	Thr	Ser	Leu	Ser	Arg	Asp	Cys	Asn		
		355					360					365					
Thr	Cys	Ile	Cys	Arg	Asn	Ser	Gln	Trp	Ile	Cys	Ser	Asn	Glu	Glu	Cys		
	370					375					380						
Pro	Gly	Glu	Cys	Leu	Val	Thr	Gly	Gln	Ser	His	Phe	Lys	Ser	Phe	Asp		
385					390					395					400		
Asn	Arg	Tyr	Phe	Thr	Phe	Ser	Gly	Ile	Cys	Gln	Tyr	Leu	Leu	Ala	Arg		
				405					410					415			
Asp	Cys	Gln	Asp	His	Ser	Phe	Ser	Ile	Val	Ile	Glu	Thr	Val	Gln	Cys		
			420					425					430				
Ala	Asp	Asp	Arg	Asp	Ala	Val	Cys	Thr	Arg	Ser	Val	Thr	Val	Arg	Leu		
		435					440					445					
Pro	Gly	Leu	His	Asn	Ser	Leu	Val	Lys	Leu	Lys	His	Gly	Ala	Gly	Val		
	450					455					460						
Ala	Met	Asp	Gly	Gln	Asp	Val	Gln	Leu	Pro	Leu	Leu	Lys	Gly	Asp	Leu		
465					470					475					480		
Arg	Ile	Gln	His	Thr	Val	Thr	Ala	Ser	Val	Arg	Leu	Ser	Tyr	Gly	Glu		
				485					490						495		
Asp	Leu	Gln	Met	Asp	Trp	Asp	Gly	Arg	Gly	Arg	Leu	Leu	Val	Lys	Leu		
			500					505					510				
Ser	Pro	Val	Tyr	Ala	Gly	Lys	Thr	Cys	Gly	Leu	Cys	Gly	Asn	Tyr	Asn		
		515					520					525					
Gly	Asn	Gln	Gly	Asp	Asp	Phe	Leu	Thr	Pro	Ser	Gly	Leu	Ala	Glu	Pro		
	530					535					540						
Arg	Val	Glu	Asp	Phe	Gly	Asn	Ala	Trp	Lys	Leu	His	Gly	Asp	Cys	Gln		
545					550					555					560		
Asp	Leu	Gln	Lys	Gln	His	Ser	Asp	Pro	Cys	Ala	Leu	Asn	Pro	Arg	Met		
				565					570						575		
Thr	Arg	Phe	Ser	Glu	Glu	Ala	Cys	Ala	Val	Leu	Thr	Ser	Pro	Thr	Phe		
			580					585					590				
Glu	Ala	Cys	His	Arg	Ala	Val	Ser	Pro	Leu	Pro	Tyr	Leu	Arg	Asn	Cys		
		595					600					605					
Arg	Tyr	Asp	Val	Cys	Ser	Cys	Ser	Asp	Gly	Arg	Glu	Cys	Leu	Cys	Gly		
	610					615					620						
Ala	Leu	Ala	Ser	Tyr	Ala	Ala	Ala	Cys	Ala	Gly	Arg	Gly	Val	Arg	Val		
625					630					635					640		
Ala	Trp	Arg	Glu	Pro	Gly	Arg	Cys	Glu	Leu	Asn	Cys	Pro	Lys	Gly	Gln		
				645					650						655		
Val	Tyr	Leu	Gln	Cys	Gly	Thr	Pro	Cys	Asn	Leu	Thr	Cys	Arg	Ser	Leu		
			660					665					670				
Ser	Tyr	Pro	Asp	Glu	Glu	Cys	Asn	Glu	Ala	Cys	Leu	Glu	Gly	Cys	Phe		
		675					680					685					
Cys	Pro	Pro	Gly	Leu	Tyr	Met	Asp	Glu	Arg	Gly	Asp	Cys	Val	Pro	Lys		
	690					695					700						
Ala	Gln	Cys	Pro	Cys	Tyr	Tyr	Asp	Gly	Glu	Ile	Phe	Gln	Pro	Glu	Asp		
705					710					715					720		
Ile	Phe	Ser	Asp	His	His	Thr	Met	Cys	Tyr	Cys	Glu	Asp	Gly	Phe	Met		
				725					730					735			

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His Cys Thr Met Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val
 740 745 750
 Leu Ser Ser Pro Leu Ser His Arg Ser Lys Arg Ser Leu Ser Cys Arg
 755 760 765
 Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Leu Arg Ala Glu
 770 775 780
 Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr Asp Leu Glu Cys Met
 785 790 795 800
 Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro Pro Gly Met Val Arg
 805 810 815
 His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
 820 825 830
 Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Gly Cys Asn Thr
 835 840 845
 Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr Asp His Val Cys Asp
 850 855 860
 Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
 865 870 875 880
 Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
 885 890 895
 Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
 900 905 910
 Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
 915 920 925
 Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
 930 935 940
 Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
 945 950 955 960
 Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
 965 970 975
 His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
 980 985 990
 Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln Asn Asn Asp Leu Thr
 995 1000 1005
 Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val Asp Phe Gly Asn
 1010 1015 1020
 Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg Lys Val Pro
 1025 1030 1035
 Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met Lys Gln
 1040 1045 1050
 Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val Phe
 1055 1060 1065
 Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val
 1070 1075 1080
 Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala
 1085 1090 1095
 Cys Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln
 1100 1105 1110
 His Gly Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln
 1115 1120 1125
 Ser Cys Glu Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu Cys Glu
 1130 1135 1140

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Trp	Arg	Tyr	Asn	Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln
1145						1150					1155			
His	Pro	Glu	Pro	Leu	Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys
1160						1165					1170			
His	Ala	His	Cys	Pro	Pro	Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln
1175						1180					1185			
Thr	Cys	Val	Asp	Pro	Glu	Asp	Cys	Pro	Val	Cys	Glu	Val	Ala	Gly
1190						1195					1200			
Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys	Val	Thr	Leu	Asn	Pro	Ser	Asp
1205						1210					1215			
Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys	Asp	Val	Val	Asn	Leu	Thr
1220						1225					1230			
Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	Leu	Val	Val	Pro	Pro	Thr
1235						1240					1245			
Asp	Ala	Pro	Val	Ser	Pro	Thr	Thr	Leu	Tyr	Val	Glu	Asp	Ile	Ser
1250						1255					1260			
Glu	Pro	Pro	Leu	His	Asp	Phe	Tyr	Cys	Ser	Arg	Leu	Leu	Asp	Leu
1265						1270					1275			
Val	Phe	Leu	Leu	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Glu	Ala	Glu	Phe
1280						1285					1290			
Glu	Val	Leu	Lys	Ala	Phe	Val	Val	Asp	Met	Met	Glu	Arg	Leu	Arg
1295						1300					1305			
Ile	Ser	Gln	Lys	Trp	Val	Arg	Val	Ala	Val	Val	Glu	Tyr	His	Asp
1310						1315					1320			
Gly	Ser	His	Ala	Tyr	Ile	Gly	Leu	Lys	Asp	Arg	Lys	Arg	Pro	Ser
1325						1330					1335			
Glu	Leu	Arg	Arg	Ile	Ala	Ser	Gln	Val	Lys	Tyr	Ala	Gly	Ser	Gln
1340						1345					1350			
Val	Ala	Ser	Thr	Ser	Glu	Val	Leu	Lys	Tyr	Thr	Leu	Phe	Gln	Ile
1355						1360					1365			
Phe	Ser	Lys	Ile	Asp	Arg	Pro	Glu	Ala	Ser	Arg	Ile	Thr	Leu	Leu
1370						1375					1380			
Leu	Met	Ala	Ser	Gln	Glu	Pro	Gln	Arg	Met	Ser	Arg	Asn	Phe	Val
1385						1390					1395			
Arg	Tyr	Val	Gln	Gly	Leu	Lys	Lys	Lys	Lys	Val	Ile	Val	Ile	Pro
1400						1405					1410			
Val	Gly	Ile	Gly	Pro	His	Ala	Asn	Leu	Lys	Gln	Ile	Arg	Leu	Ile
1415						1420					1425			
Glu	Lys	Gln	Ala	Pro	Glu	Asn	Lys	Ala	Phe	Val	Leu	Ser	Ser	Val
1430						1435					1440			
Asp	Glu	Leu	Glu	Gln	Gln	Arg	Asp	Glu	Ile	Val	Ser	Tyr	Leu	Cys
1445						1450					1455			
Asp	Leu	Ala	Pro	Glu	Ala	Pro	Pro	Pro	Thr	Leu	Pro	Pro	Asp	Met
1460						1465					1470			
Ala	Gln	Val	Thr	Val	Gly	Pro	Gly	Leu	Leu	Gly	Val	Ser	Thr	Leu
1475						1480					1485			
Gly	Pro	Lys	Arg	Asn	Ser	Met	Val	Leu	Asp	Val	Ala	Phe	Val	Leu
1490						1495					1500			
Glu	Gly	Ser	Asp	Lys	Ile	Gly	Glu	Ala	Asp	Phe	Asn	Arg	Ser	Lys
1505						1510					1515			
Glu	Phe	Met	Glu	Glu	Val	Ile	Gln	Arg	Met	Asp	Val	Gly	Gln	Asp
1520						1525					1530			
Ser	Ile	His	Val	Thr	Val	Leu	Gln	Tyr	Ser	Tyr	Met	Val	Thr	Val

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1535	1540	1545
Glu Tyr Pro Phe Ser Glu Ala Gln Ser Lys Gly Asp Ile Leu Gln 1550 1555 1560		
Arg Val Arg Glu Ile Arg Tyr Gln Gly Gly Asn Arg Thr Asn Thr 1565 1570 1575		
Gly Leu Ala Leu Arg Tyr Leu Ser Asp His Ser Phe Leu Val Ser 1580 1585 1590		
Gln Gly Asp Arg Glu Gln Ala Pro Asn Leu Val Tyr Met Val Thr 1595 1600 1605		
Gly Asn Pro Ala Ser Asp Glu Ile Lys Arg Leu Pro Gly Asp Ile 1610 1615 1620		
Gln Val Val Pro Ile Gly Val Gly Pro Asn Ala Asn Val Gln Glu 1625 1630 1635		
Leu Glu Arg Ile Gly Trp Pro Asn Ala Pro Ile Leu Ile Gln Asp 1640 1645 1650		
Phe Glu Thr Leu Pro Arg Glu Ala Pro Asp Leu Val Leu Gln Arg 1655 1660 1665		
Cys Cys Ser Gly Glu Gly Leu Gln Ile Pro Thr Leu Ser Pro Ala 1670 1675 1680		
Pro Asp Cys Ser Gln Pro Leu Asp Val Ile Leu Leu Leu Asp Gly 1685 1690 1695		
Ser Ser Ser Phe Pro Ala Ser Tyr Phe Asp Glu Met Lys Ser Phe 1700 1705 1710		
Ala Lys Ala Phe Ile Ser Lys Ala Asn Ile Gly Pro Arg Leu Thr 1715 1720 1725		
Gln Val Ser Val Leu Gln Tyr Gly Ser Ile Thr Thr Ile Asp Val 1730 1735 1740		
Pro Trp Asn Val Val Pro Glu Lys Ala His Leu Leu Ser Leu Val 1745 1750 1755		
Asp Val Met Gln Arg Glu Gly Gly Pro Ser Gln Ile Gly Asp Ala 1760 1765 1770		
Leu Gly Phe Ala Val Arg Tyr Leu Thr Ser Glu Met His Gly Ala 1775 1780 1785		
Arg Pro Gly Ala Ser Lys Ala Val Val Ile Leu Val Thr Asp Val 1790 1795 1800		
Ser Val Asp Ser Val Asp Ala Ala Ala Asp Ala Ala Arg Ser Asn 1805 1810 1815		
Arg Val Thr Val Phe Pro Ile Gly Ile Gly Asp Arg Tyr Asp Ala 1820 1825 1830		
Ala Gln Leu Arg Ile Leu Ala Gly Pro Ala Gly Asp Ser Asn Val 1835 1840 1845		
Val Lys Leu Gln Arg Ile Glu Asp Leu Pro Thr Met Val Thr Leu 1850 1855 1860		
Gly Asn Ser Phe Leu His Lys Leu Cys Ser Gly Phe Val Arg Ile 1865 1870 1875		
Cys Met Asp Glu Asp Gly Asn Glu Lys Arg Pro Gly Asp Val Trp 1880 1885 1890		
Thr Leu Pro Asp Gln Cys His Thr Val Thr Cys Gln Pro Asp Gly 1895 1900 1905		
Gln Thr Leu Leu Lys Ser His Arg Val Asn Cys Asp Arg Gly Leu 1910 1915 1920		
Arg Pro Ser Cys Pro Asn Ser Gln Ser Pro Val Lys Val Glu Glu 1925 1930 1935		

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Thr Cys Gly Cys Arg Trp Thr Cys Pro Cys Val Cys Thr Gly Ser 1940 1945 1950	
Ser Thr Arg His Ile Val Thr Phe Asp Gly Gln Asn Phe Lys Leu 1955 1960 1965	
Thr Gly Ser Cys Ser Tyr Val Leu Phe Gln Asn Lys Glu Gln Asp 1970 1975 1980	
Leu Glu Val Ile Leu His Asn Gly Ala Cys Ser Pro Gly Ala Arg 1985 1990 1995	
Gln Gly Cys Met Lys Ser Ile Glu Val Lys His Ser Ala Leu Ser 2000 2005 2010	
Val Glu Leu His Ser Asp Met Glu Val Thr Val Asn Gly Arg Leu 2015 2020 2025	
Val Ser Val Pro Tyr Val Gly Gly Asn Met Glu Val Asn Val Tyr 2030 2035 2040	
Gly Ala Ile Met His Glu Val Arg Phe Asn His Leu Gly His Ile 2045 2050 2055	
Phe Thr Phe Thr Pro Gln Asn Asn Glu Phe Gln Leu Gln Leu Ser 2060 2065 2070	
Pro Lys Thr Phe Ala Ser Lys Thr Tyr Gly Leu Cys Gly Ile Cys 2075 2080 2085	
Asp Glu Asn Gly Ala Asn Asp Phe Met Leu Arg Asp Gly Thr Val 2090 2095 2100	
Thr Thr Asp Trp Lys Thr Leu Val Gln Glu Trp Thr Val Gln Arg 2105 2110 2115	
Pro Gly Gln Thr Cys Gln Pro Ile Leu Glu Glu Gln Cys Leu Val 2120 2125 2130	
Pro Asp Ser Ser His Cys Gln Val Leu Leu Leu Pro Leu Phe Ala 2135 2140 2145	
Glu Cys His Lys Val Leu Ala Pro Ala Thr Phe Tyr Ala Ile Cys 2150 2155 2160	
Gln Gln Asp Ser Cys His Gln Glu Gln Val Cys Glu Val Ile Ala 2165 2170 2175	
Ser Tyr Ala His Leu Cys Arg Thr Asn Gly Val Cys Val Asp Trp 2180 2185 2190	
Arg Thr Pro Asp Phe Cys Ala Met Ser Cys Pro Pro Ser Leu Val 2195 2200 2205	
Tyr Asn His Cys Glu His Gly Cys Pro Arg His Cys Asp Gly Asn 2210 2215 2220	
Val Ser Ser Cys Gly Asp His Pro Ser Glu Gly Cys Phe Cys Pro 2225 2230 2235	
Pro Asp Lys Val Met Leu Glu Gly Ser Cys Val Pro Glu Glu Ala 2240 2245 2250	
Cys Thr Gln Cys Ile Gly Glu Asp Gly Val Gln His Gln Phe Leu 2255 2260 2265	
Glu Ala Trp Val Pro Asp His Gln Pro Cys Gln Ile Cys Thr Cys 2270 2275 2280	
Leu Ser Gly Arg Lys Val Asn Cys Thr Thr Gln Pro Cys Pro Thr 2285 2290 2295	
Ala Lys Ala Pro Thr Cys Gly Leu Cys Glu Val Ala Arg Leu Arg 2300 2305 2310	
Gln Asn Ala Asp Gln Cys Cys Pro Glu Tyr Glu Cys Val Cys Asp 2315 2320 2325	

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Pro Val	Ser Cys Asp	Leu Pro	Pro Val	Pro His	Cys	Glu Arg Gly
2330		2335			2340	
Leu Gln	Pro Thr Leu Thr	Asn	Pro Gly	Glu Cys Arg	Pro Asn Phe	
2345		2350		2355		
Thr Cys	Ala Cys Arg Lys	Glu	Glu Cys Lys Arg	Val	Ser Pro Pro	
2360		2365		2370		
Ser Cys	Pro Pro His Arg	Leu	Pro Thr Leu Arg	Lys	Thr Gln Cys	
2375		2380		2385		
Cys Asp	Glu Tyr Glu Cys	Ala	Cys Asn Cys Val	Asn	Ser Thr Val	
2390		2395		2400		
Ser Cys	Pro Leu Gly Tyr	Leu	Ala Ser Thr Ala	Thr	Asn Asp Cys	
2405		2410		2415		
Gly Cys	Thr Thr Thr Thr	Cys	Leu Pro Asp Lys	Val	Cys Val His	
2420		2425		2430		
Arg Ser	Thr Ile Tyr Pro	Val	Gly Gln Phe Trp	Glu	Glu Gly Cys	
2435		2440		2445		
Asp Val	Cys Thr Cys Thr	Asp	Met Glu Asp Ala	Val	Met Gly Leu	
2450		2455		2460		
Arg Val	Ala Gln Cys Ser	Gln	Lys Pro Cys Glu	Asp	Ser Cys Arg	
2465		2470		2475		
Ser Gly	Phe Thr Tyr Val	Leu	His Glu Gly Glu	Cys	Cys Gly Arg	
2480		2485		2490		
Cys Leu	Pro Ser Ala Cys	Glu	Val Val Thr Gly	Ser	Pro Arg Gly	
2495		2500		2505		
Asp Ser	Gln Ser Ser Trp	Lys	Ser Val Gly Ser	Gln	Trp Ala Ser	
2510		2515		2520		
Pro Glu	Asn Pro Cys Leu	Ile	Asn Glu Cys Val	Arg	Val Lys Glu	
2525		2530		2535		
Glu Val	Phe Ile Gln Gln	Arg	Asn Val Ser Cys	Pro	Gln Leu Glu	
2540		2545		2550		
Val Pro	Val Cys Pro Ser	Gly	Phe Gln Leu Ser	Cys	Lys Thr Ser	
2555		2560		2565		
Ala Cys	Cys Pro Ser Cys	Arg	Cys Glu Arg Met	Glu	Ala Cys Met	
2570		2575		2580		
Leu Asn	Gly Thr Val Ile	Gly	Pro Gly Lys Thr	Val	Met Ile Asp	
2585		2590		2595		
Val Cys	Thr Thr Cys Arg	Cys	Met Val Gln Val	Gly	Val Ile Ser	
2600		2605		2610		
Gly Phe	Lys Leu Glu Cys	Arg	Lys Thr Thr Cys	Asn	Pro Cys Pro	
2615		2620		2625		
Leu Gly	Tyr Lys Glu Glu	Asn	Asn Thr Gly Glu	Cys	Cys Gly Arg	
2630		2635		2640		
Cys Leu	Pro Thr Ala Cys	Thr	Ile Gln Leu Arg	Gly	Gly Gln Ile	
2645		2650		2655		
Met Thr	Leu Lys Arg Asp	Glu	Thr Leu Gln Asp	Gly	Cys Asp Thr	
2660		2665		2670		
His Phe	Cys Lys Val Asn	Glu	Arg Gly Glu Tyr	Phe	Trp Glu Lys	
2675		2680		2685		
Arg Val	Thr Gly Cys Pro	Pro	Phe Asp Glu His	Lys	Cys Leu Ala	
2690		2695		2700		
Glu Gly	Gly Lys Ile Met	Lys	Ile Pro Gly Thr	Cys	Cys Asp Thr	
2705		2710		2715		
Cys Glu	Glu Pro Glu Cys	Asn	Asp Ile Thr Ala	Arg	Leu Gln Tyr	

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2720	2725	2730
Val Lys Val Gly Ser Cys Lys Ser Glu Val Glu Val Asp Ile His		
2735	2740	2745
Tyr Cys Gln Gly Lys Cys Ala Ser Lys Ala Met Tyr Ser Ile Asp		
2750	2755	2760
Ile Asn Asp Val Gln Asp Gln Cys Ser Cys Cys Ser Pro Thr Arg		
2765	2770	2775
Thr Glu Pro Met Gln Val Ala Leu His Cys Thr Asn Gly Ser Val		
2780	2785	2790
Val Tyr His Glu Val Leu Asn Ala Met Glu Cys Lys Cys Ser Pro		
2795	2800	2805
Arg Lys Cys Ser Lys		
2810		

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<210> SEQ ID NO 24
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<400> SEQUENCE: 24

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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 25

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<210> SEQ ID NO 26
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 <220> FEATURE:
 <223> OTHER INFORMATION: Reverse primer JP1003 VWF 764-1035

<400> SEQUENCE: 26

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<210> SEQ ID NO 27
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Reverse primer JP1004 VWF 764-1041

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<210> SEQ ID NO 28
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Reverse primer JP1005 VWF 764-1045

<400> SEQUENCE: 28

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<210> SEQ ID NO 29
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Reverse primer JP1006 VWF 764-1250

<400> SEQUENCE: 29

tggtcctcag ctagcgcggt atctgtggga ggcaccacc 39

<210> SEQ ID NO 30
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Reverse primer JP1007 VWF 764-1261

<400> SEQUENCE: 30

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Reverse primer JP1008 VWF 764-1268

<400> SEQUENCE: 31

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VWF(864-1250)-HPC4 S

<400> SEQUENCE: 32

gggacccttt gtgatgccac gtgctccacg atcgg 35

<210> SEQ ID NO 33
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VWF(864-1250)-HPC4 AS

<400> SEQUENCE: 33

gcacgtggca tcacaaaggg tccctggcaa aatgag 36

<210> SEQ ID NO 34
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: VWF(764-1128)-HPC4 S

<400> SEQUENCE: 34

ttgtgcccc aggaggacca agtagatccg cggctc 36

<210> SEQ ID NO 35
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VWF(764-1129)-HPC4 AS

<400> SEQUENCE: 35

tacttggtcc tctgggggc acaatgtggc cgtc 34

<210> SEQ ID NO 36
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VWF(764-1198)-HPC4 S

<400> SEQUENCE: 36

gactgtccag tggaggacca agtagatccg cgg 33

<210> SEQ ID NO 37
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VWF(764-1198)-HPC4 AS

<400> SEQUENCE: 37

ttggtctcc actggacagt cttcagggtc aa 32

<210> SEQ ID NO 38
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HPC4 tag

<400> SEQUENCE: 38

Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys
1 5 10

<210> SEQ ID NO 39
<211> LENGTH: 100
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oLLC089 VWF forward

<400> SEQUENCE: 39

ccgctagccc atgattcctg ccagatttgc cggggtgctg cttgctctgg ccctcatttt 60

gccagggacc cttttagacc tatectgtcg gcccccatg 100

<210> SEQ ID NO 40
<211> LENGTH: 85
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oLLC092 VWF A1 HPC4 reverse

<400> SEQUENCE: 40

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gatgcggcgcg cctactacta ttgccatca atcagacgcg gatccacctg atcttcgget	60
tcagggggcaa ggtcacagag gtagc	85

<210> SEQ ID NO 41
 <211> LENGTH: 40
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: oLLC101-f

<400> SEQUENCE: 41

cattggggac tgcgcctcct tctgcgacac cattgctgcc	40
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<210> SEQ ID NO 42
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: oLLC102-r

<400> SEQUENCE: 42

ggcagcaatg gtgtcgcaga aggaggcgca gtccccaatg	40
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<210> SEQ ID NO 43
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
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<400> SEQUENCE: 43

cgggagaacg ggtatgagtc tgagtggcgc tataacagct gtgc	44
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<210> SEQ ID NO 44
 <211> LENGTH: 44
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: oLLC104-r

<400> SEQUENCE: 44

gcacagctgt tatagcgcca ctcagactca taccggttct cccg	44
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<210> SEQ ID NO 45
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: VWF 1099C S

<400> SEQUENCE: 45

ggggactgcg cctgcttctg cgacacc	27
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<210> SEQ ID NO 46
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: VWF 1099C AS

<400> SEQUENCE: 46

ggtgtcgcag aagcaggcgc agtcccc	27
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<210> SEQ ID NO 47
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VWF 1142C S

<400> SEQUENCE: 47

gaacgggtat gagtgtgagt ggcgctata 29

<210> SEQ ID NO 48
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 48

tatagcgcca ctcacactca taccggttc 29

<210> SEQ ID NO 49
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 2764pJSV348F

<400> SEQUENCE: 49

gcgctagctg aggaccaagt agatccgcgg ctcattgatg gg 42

<210> SEQ ID NO 50
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: 1202pJSV348R

<400> SEQUENCE: 50

gggccagagc aagcagcacc ccggcaaadc tggcagg 37

<210> SEQ ID NO 51
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 221 796F

<400> SEQUENCE: 51

cctgccagat ttgccggggt gctgcttgct ctggccc 37

<210> SEQ ID NO 52
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: 3537 796R

<400> SEQUENCE: 52

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: 3747 796R

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<400> SEQUENCE: 53

tacttggtcc tcagctagcg ccactggaca gtottcaggg tcaacgc

47

<210> SEQ ID NO 54

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 2420pJSV348R

<400> SEQUENCE: 54

ggctcagggt gctgacacgt gacttgacag gcaggtgc

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<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 3666 796F

<400> SEQUENCE: 55

gcacctgcct gtcaagtcac gtgtcagcac cctgagcc

38

<210> SEQ ID NO 56

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 5203 796R

<400> SEQUENCE: 56

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46

<210> SEQ ID NO 57

<211> LENGTH: 479

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: VWF fragment: amino acids 764-1242

<400> SEQUENCE: 57

Ser	Leu	Ser	Cys	Arg	Pro	Pro	Met	Val	Lys	Leu	Val	Cys	Pro	Ala	Asp
1			5						10					15	

Asn	Leu	Arg	Ala	Glu	Gly	Leu	Glu	Cys	Thr	Lys	Thr	Cys	Gln	Asn	Tyr
		20						25					30		

Asp	Leu	Glu	Cys	Met	Ser	Met	Gly	Cys	Val	Ser	Gly	Cys	Leu	Cys	Pro
		35					40					45			

Pro	Gly	Met	Val	Arg	His	Glu	Asn	Arg	Cys	Val	Ala	Leu	Glu	Arg	Cys
		50				55					60				

Pro	Cys	Phe	His	Gln	Gly	Lys	Glu	Tyr	Ala	Pro	Gly	Glu	Thr	Val	Lys
65				70					75					80	

Ile	Gly	Cys	Asn	Thr	Cys	Val	Cys	Gln	Asp	Arg	Lys	Trp	Asn	Cys	Thr
			85						90					95	

Asp	His	Val	Cys	Asp	Ala	Thr	Cys	Ser	Thr	Ile	Gly	Met	Ala	His	Tyr
			100					105					110		

Leu	Thr	Phe	Asp	Gly	Leu	Lys	Tyr	Leu	Phe	Pro	Gly	Glu	Cys	Gln	Tyr
		115				120						125			

Val	Leu	Val	Gln	Asp	Tyr	Cys	Gly	Ser	Asn	Pro	Gly	Thr	Phe	Arg	Ile
		130				135					140				

Leu	Val	Gly	Asn	Lys	Gly	Cys	Ser	His	Pro	Ser	Val	Lys	Cys	Lys	Lys
145					150					155					160

Arg	Val	Thr	Ile	Leu	Val	Glu	Gly	Gly	Glu	Ile	Glu	Leu	Phe	Asp	Gly
			165						170					175	
Glu	Val	Asn	Val	Lys	Arg	Pro	Met	Lys	Asp	Glu	Thr	His	Phe	Glu	Val
		180						185					190		
Val	Glu	Ser	Gly	Arg	Tyr	Ile	Ile	Leu	Leu	Leu	Gly	Lys	Ala	Leu	Ser
		195					200					205			
Val	Val	Trp	Asp	Arg	His	Leu	Ser	Ile	Ser	Val	Val	Leu	Lys	Gln	Thr
	210					215				220					
Tyr	Gln	Glu	Lys	Val	Cys	Gly	Leu	Cys	Gly	Asn	Phe	Asp	Gly	Ile	Gln
225					230					235					240
Asn	Asn	Asp	Leu	Thr	Ser	Ser	Asn	Leu	Gln	Val	Glu	Glu	Asp	Pro	Val
				245					250					255	
Asp	Phe	Gly	Asn	Ser	Trp	Lys	Val	Ser	Ser	Gln	Cys	Ala	Asp	Thr	Arg
			260					265					270		
Lys	Val	Pro	Leu	Asp	Ser	Ser	Pro	Ala	Thr	Cys	His	Asn	Asn	Ile	Met
		275					280					285			
Lys	Gln	Thr	Met	Val	Asp	Ser	Ser	Cys	Arg	Ile	Leu	Thr	Ser	Asp	Val
	290				295						300				
Phe	Gln	Asp	Cys	Asn	Lys	Leu	Val	Asp	Pro	Glu	Pro	Tyr	Leu	Asp	Val
305					310					315					320
Cys	Ile	Tyr	Asp	Thr	Cys	Ser	Cys	Glu	Ser	Ile	Gly	Asp	Cys	Ala	Cys
				325					330					335	
Phe	Cys	Asp	Thr	Ile	Ala	Ala	Tyr	Ala	His	Val	Cys	Ala	Gln	His	Gly
			340					345					350		
Lys	Val	Val	Thr	Trp	Arg	Thr	Ala	Thr	Leu	Cys	Pro	Gln	Ser	Cys	Glu
		355					360					365			
Glu	Arg	Asn	Leu	Arg	Glu	Asn	Gly	Tyr	Glu	Cys	Glu	Trp	Arg	Tyr	Asn
	370					375					380				
Ser	Cys	Ala	Pro	Ala	Cys	Gln	Val	Thr	Cys	Gln	His	Pro	Glu	Pro	Leu
385					390					395					400
Ala	Cys	Pro	Val	Gln	Cys	Val	Glu	Gly	Cys	His	Ala	His	Cys	Pro	Pro
				405					410					415	
Gly	Lys	Ile	Leu	Asp	Glu	Leu	Leu	Gln	Thr	Cys	Val	Asp	Pro	Glu	Asp
			420					425					430		
Cys	Pro	Val	Cys	Glu	Val	Ala	Gly	Arg	Arg	Phe	Ala	Ser	Gly	Lys	Lys
		435					440					445			
Val	Thr	Leu	Asn	Pro	Ser	Asp	Pro	Glu	His	Cys	Gln	Ile	Cys	His	Cys
	450					455					460				
Asp	Val	Val	Asn	Leu	Thr	Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	
465					470					475					

Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp
 1 5 10 15
 Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr
 20 25 30
 Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro
 35 40 45

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Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys	
50	55 60
Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys	
65	70 75 80
Ile Gly Cys Asn Thr Cys Val Cys Gln Asp Arg Lys Trp Asn Cys Thr	
	85 90 95
Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr	
	100 105 110
Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr	
	115 120 125
Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile	
	130 135 140
Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys	
145	150 155 160
Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly	
	165 170 175
Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe Glu Val	
	180 185 190
Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser	
	195 200 205
Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys Gln Thr	
	210 215 220
Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln	
225	230 235 240
Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val	
	245 250 255
Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg	
	260 265 270
Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met	
	275 280 285
Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val	
	290 295 300
Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val	
305	310 315 320
Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala Cys	
	325 330 335
Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln His Gly	
	340 345 350
Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln Ser Cys Glu	
	355 360 365
Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu Cys Glu Trp Arg Tyr Asn	
	370 375 380
Ser Cys Ala Pro Ala Cys Gln Val Thr Cys Gln His Pro Glu Pro Leu	
385	390 395 400
Ala Cys Pro Val Gln Cys Val Glu Gly Cys His Ala His Cys Pro Pro	
	405 410 415
Gly Lys Ile Leu Asp Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp	
	420 425 430
Cys Pro Val Cys Glu Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys	
	435 440 445
Val Thr Leu Asn Pro Ser Asp Pro Glu His Cys Gln Ile Cys His Cys	
	450 455 460

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Asp	Val	Val	Asn	Leu	Thr	Cys	Glu	Ala	Cys	Gln	Glu	Pro	Gly	Gly	Leu	465	470	475	480
Val	Val	Pro	Pro	Thr	Asp	Ala	Pro	Val	Ser	Pro	Thr	Thr	Leu	Tyr	Val	485	490	495	
Glu	Asp	Ile	Ser	Glu	Pro	Pro	Leu	His	Asp	Phe	Tyr	Cys	Ser	Arg	Leu	500	505	510	
Leu	Asp	Leu	Val	Phe	Leu	Leu	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Glu	Ala	515	520	525	
Glu	Phe	Glu	Val	Leu	Lys	Ala	Phe	Val	Val	Asp	Met	Met	Glu	Arg	Leu	530	535	540	
Arg	Ile	Ser	Gln	Lys	Trp	Val	Arg	Val	Ala	Val	Val	Glu	Tyr	His	Asp	545	550	555	560
Gly	Ser	His	Ala	Tyr	Ile	Gly	Leu	Lys	Asp	Arg	Lys	Arg	Pro	Ser	Glu	565	570	575	
Leu	Arg	Arg	Ile	Ala	Ser	Gln	Val	Lys	Tyr	Ala	Gly	Ser	Gln	Val	Ala	580	585	590	
Ser	Thr	Ser	Glu	Val	Leu	Lys	Tyr	Thr	Leu	Phe	Gln	Ile	Phe	Ser	Lys	595	600	605	
Ile	Asp	Arg	Pro	Glu	Ala	Ser	Arg	Ile	Thr	Leu	Leu	Leu	Met	Ala	Ser	610	615	620	
Gln	Glu	Pro	Gln	Arg	Met	Ser	Arg	Asn	Phe	Val	Arg	Tyr	Val	Gln	Gly	625	630	635	640
Leu	Lys	Lys	Lys	Lys	Val	Ile	Val	Ile	Pro	Val	Gly	Ile	Gly	Pro	His	645	650	655	
Ala	Asn	Leu	Lys	Gln	Ile	Arg	Leu	Ile	Glu	Lys	Gln	Ala	Pro	Glu	Asn	660	665	670	
Lys	Ala	Phe	Val	Leu	Ser	Ser	Val	Asp	Glu	Leu	Glu	Gln	Gln	Arg	Asp	675	680	685	
Glu	Ile	Val	Ser	Tyr	Leu	Cys	Asp	Leu	Ala	Pro	Glu	Ala	Pro	Pro	Pro	690	695	700	
Thr	Leu	Pro	Pro	Asp	Met	Ala	Gln	Val	Thr	Val	Gly	Pro	Gly	Leu		705	710	715	

The invention claimed is:

1. A pharmaceutical composition comprising: (i) a Von Willebrand Factor (VWF) fragment comprising up to 800 amino acids and one or more domains selected from the group consisting of trypsin-inhibitor-like (TIL'), E', and D3 and (ii) a B domain-truncated Factor VIII molecule with an amino acid sequence comprising SEQ ID NO:2, wherein SEQ ID NO:2 is modified by a deletion of its C-terminal R.

2. The pharmaceutical composition according to claim 1, wherein the amino acid sequence of the B domain-truncated Factor VIII from N-terminal to C-terminal consists of amino acid residues 1-750, 1638-1647, and 1649-2332 of SEQ ID NO: 1 and, wherein an O-glycan is linked to the Ser 750 amino acid residue.

3. The pharmaceutical composition according to claim 1, wherein the B domain-truncated Factor VIII molecule is conjugated with at least one half-life extending moiety.

4. The pharmaceutical composition according to claim 3, wherein the at least one half-life extending moiety is covalently attached to an O-glycan linked to the B domain-truncated Factor VIII molecule at an amino acid residue within the amino acid sequence represented by SEQ ID NO:2, wherein SEQ ID NO:2 is modified by the deletion of the C-terminal R.

5. The pharmaceutical composition according to claim 1, wherein the bioavailability of the B domain-truncated Factor VIII molecule is at least 5% following subcutaneous administration.

6. The pharmaceutical composition according to claim 1, wherein the molar ratio between the B domain-truncated Factor VIII molecule and VWF is 1:1.

7. The pharmaceutical composition according to claim 1, wherein the concentration of the B domain-truncated Factor VIII molecule is at least 500 IU/ml.

8. The pharmaceutical composition according to claim 1, wherein the amount of the B domain-truncated Factor VIII molecule bound to the VWF fragment is at least 70% of the total amount of B domain-truncated the Factor VIII molecule in said composition.

9. The pharmaceutical composition according to claim 1 for use in treating haemophilia, wherein said pharmaceutical composition is for subcutaneous administration.

10. The pharmaceutical composition according to claim 1 for use in treating haemophilia, wherein said pharmaceutical composition is for intravenous administration.

11. The pharmaceutical composition according to claim 1 for use in treating haemophilia, wherein said pharmaceutical composition is a freeze-dried composition.

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12. The pharmaceutical composition according to claim 1 for use in treating haemophilia, wherein said pharmaceutical composition is a liquid composition.

13. The pharmaceutical composition according to claim 1, wherein the amino acid sequence of the VWF fragment is selected from the group consisting of: SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, and SEQ ID NO: 58.

14. The pharmaceutical composition according to claim 1 for use in treatment of von willebrand disease by intravenous or subcutaneous administration.

15. The pharmaceutical composition according to one of claims 3 and 4, wherein the half-life extending moiety is poly(ethylene glycol).

16. A pharmaceutical composition comprising: (i) a Von Willebrand Factor (VWF) fragment comprising up to 800 amino acids and one or more domains selected from the group consisting of trypsin-inhibitor-like (TIL'), E', and D3; (ii) a B

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domain-truncated Factor VIII molecule with an amino acid sequence from N-terminal to C-terminal consisting of amino acid residues 1-750, 1638-1647, and 1649-2332 of SEQ ID NO: 1 and (iii) a poly(ethylene glycol) moiety attached to the B domain-truncated Factor VIII molecule via an O-glycan linked to the Ser 750 amino acid residue.

17. The pharmaceutical composition according to claim 16, wherein the VWF fragment is selected from the group consisting of: SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, and SEQ ID NO: 58.

18. The pharmaceutical composition according to claim 17, wherein the VWF fragment is SEQ ID NO: 19.

19. The pharmaceutical composition according to claim 16, wherein the molar ratio between the Factor VIII molecule and VWF is from 1:1 to 1:7.7.

20. The pharmaceutical composition according to claim 19, wherein the molar ratio is 1:1.

* * * * *